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Lapenotiere, Hugh
Clayton, Michael A.
Brown, Douglas R.

<120> RECOMBINANT VACCINE AGAINST BOTULINUM
NEUROTOXIN

<130> A33626 067252.0105

<140> 09/611,419

<141> 2000-07-06

<150> PCT/US00/12890

<151> 2000-05-12

<150> 60/133,865

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<151> 1999-05-12

<150> 60/146,192

<151> 1999-07-29

<160> 42

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1332

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (13) ... (1326)

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Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn

1

5

10

atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg 99

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Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
 15 20 25
 atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt 147
 Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
 30 35 40 45
 aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa 195
 Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
 50 55 60
 tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct 243
 Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
 65 70 75
 atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac 291
 Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
 80 85 90
 ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg 339
 Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
 95 100 105
 gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc 387
 Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
 110 115 120 125
 tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa 435
 Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
 130 135 140
 tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc 483
 Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
 145 150 155
 gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac 531
 Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
 160 165 170
 ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac 579
 Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His
 175 180 185
 gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac 627
 Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
 190 195 200 205
 cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac 675
 Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn
 210 215 220
 gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc 723
 Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile
 225 230 235
 ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac 771
 Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr

240	245	250	
atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta			819
Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val			
255	260	265	
ggg atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg			867
Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met			
270	275	280	285
act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc			915
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe			
	290	295	300
atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac			963
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn			
	305	310	315
aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt			1011
Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg			
	320	325	330
ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct			1059
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala			
	335	340	345
ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa			1107
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys			
	350	355	360
tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag			1155
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln			
	370	375	380
gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac			1203
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn			
	385	390	395
aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa			1251
Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu			
	400	405	410
cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat			1299
Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp			
	415	420	425
gac ggt tgg ggt gaa cgt ccg ctg taa gaattc			1332
Asp Gly Trp Gly Glu Arg Pro Leu *			
430	435		

<210> 2
 <211> 437
 <212> PRT
 <213> Artificial Sequence
 <220>

<223> Encoded polypeptide of a synthetic construct based
on BONTA Hc

<400> 2

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Thr	Ser	Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	20	25	30	
Ser	Arg	Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	35	40	45	
Pro	Ile	Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	50	55	60	
Ile	Glu	Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	65	70	75	80
Asn	Phe	Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	85	90	95	
Ile	Ser	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	100	105	110	
Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	115	120	125	
Gln	Asp	Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	130	135	140	
Met	Ile	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	145	150	155	160
Thr	Asn	Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	165	170	175	
Ile	Asp	Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	180	185	190	
Asn	Ile	Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	195	200	205	
Trp	Ile	Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	210	215	220	
Ile	Lys	Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	225	230	235	240
Phe	Trp	Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	245	250	255	
Leu	Tyr	Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	260	265	270	
Gly	Tyr	Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	275	280	285	
Ile	Tyr	Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	290	295	300	
Lys	Tyr	Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	305	310	315	320
Val	Tyr	Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	325	330	335	
Asn	Ala	Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	340	345	350	
Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	355	360	365	
Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	370	375	380	
Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	385	390	395	400
Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	405	410	415	
Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp				

420
Gly Glu Arg Pro Leu
435

425

430

<210> 3
<211> 1323
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<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (13)...(1314)

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acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg 99
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
15 20 25

tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat 147
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
30 35 40 45

ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa 195
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
50 55 60

atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa 243
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
65 70 75

aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc 291
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
80 85 90

atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat 339
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
95 100 105

tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg 387
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
110 115 120 125

cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag 435
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
130 135 140

atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc 483
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
145 150 155

acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg 531
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
160 165 170

atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat 579
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
175 180 185

aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc 627
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
190 195 200 205

tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa 675
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
210 215 220

atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac 723
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
225 230 235

ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat 771
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
240 245 250

ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc cgc 819
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
255 260 265

ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc aac 867
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
270 275 280 285

atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc aag 915
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
290 295 300

aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat cgt 963
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
305 310 315

gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct acc 1011
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
320 325 330

aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa atc 1059
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
335 340 345

ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag aac 1107
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
350 355 360 365

gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac aat 1155
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
370 375 380

ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc gct 1203

Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala		
			385					390					395				
aaa	ctg	gtt	gct	tcc	aac	tgg	tac	aat	cgt	cag	atc	gaa	cgt	tcc	tct	1251	
Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser		
		400					405					410					
cgc	act	ctg	ggc	tgc	tct	tgg	gag	ttc	atc	ccg	gtt	gat	gac	ggc	tgg	1299	
Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp		
		415				420				425							
ggc	gaa	cgt	ccg	ctg	taagaattc											1323	
Gly	Glu	Arg	Pro	Leu													
430																	

<210> 4
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BONTA Hc

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 Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
 35 40 45
 Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
 50 55 60
 Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
 65 70 75 80
 Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
 85 90 95
 Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
 100 105 110
 Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
 115 120 125
 Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
 130 135 140
 Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
 145 150 155 160
 Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
 165 170 175
 Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
 180 185 190
 Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
 195 200 205
 Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
 210 215 220
 Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
 225 230 235 240
 Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp

				245					250					255			
Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr	Met		
			260					265					270				
Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr	Leu		
		275					280					285					
Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr	Ala		
	290					295					300						
Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr	Ile		
305					310					315					320		
Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala	Ser		
				325					330					335			
Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp	Val		
			340					345					350				
Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln	Gly		
		355					360					365					
Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn	Asp		
	370					375					380						
Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu	Val		
385					390					395					400		
Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr	Leu		
				405					410					415			
Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp	Gly	Glu	Arg		
			420					425					430				
Pro	Leu																

<210> 5
 <211> 1326
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (13)...(1317)

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 1 5 10

aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac 99
 Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp
 15 20 25

ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc 147
 Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe
 30 35 40 45

gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc 195
 Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser
 50 55 60

aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac 243
 Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr

65					70					75					
gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac	291														
Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn															
80 85 90															
tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac	339														
Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn															
95 100 105															
aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act	387														
Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr															
110 115 120 125															
ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct	435														
Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser															
130 135 140															
cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc	483														
Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr															
145 150 155															
atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt	531														
Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg															
160 165 170															
ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct	579														
Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser															
175 180 185															
aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac	627														
Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr															
190 195 200 205															
atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa	675														
Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys															
210 215 220															
gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa	723														
Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys															
225 230 235															
gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg	771														
Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu															
240 245 250															
aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc	819														
Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile															
255 260 265															
cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc	867														
Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr															
270 275 280 285															
aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc	915														
Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile															
290 295 300															

aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat 963
Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp
305 310 315

cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct 1011
Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala
320 325 330

acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa 1059
Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu
335 340 345

atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag 1107
Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys
350 355 360 365

aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac 1155
Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn
370 375 380

aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc 1203
Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile
385 390 395

gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc 1251
Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser
400 405 410

tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt 1299
Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly
415 420 425

tgg ggt gaa cgt ccg ctg taagaattc 1326
Trp Gly Glu Arg Pro Leu
430 435

<210> 6

<211> 435

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 6

Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser
1 5 10 15
Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
20 25 30
Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile
35 40 45
Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu
50 55 60
Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe

65					70					75					80
Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser
				85					90					95	
Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly
			100					105					110		
Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp
		115					120					125			
Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile
	130					135					140				
Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn
145					150					155					160
Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp
			165					170					175		
Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile
			180				185					190			
Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile
		195					200					205			
Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys
	210					215					220				
Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp
225					230				235						240
Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr
			245					250					255		
Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr
			260					265					270		
Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr
		275					280					285			
Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr
	290					295					300				
Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr
305					310				315						320
Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala
			325					330					335		
Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp
			340					345					350		
Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln
		355					360					365			
Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn
	370					375					380				
Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu
385					390				395						400
Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr
			405					410					415		
Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp	Gly	Glu
			420					425					430		
Arg	Pro	Leu													
		435													

<210> 7

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (10)...(1329)

<400> 7

gaattcacg atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc 51

Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile

1

5

10

ctg aac ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac 99

Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr

15

20

25

30

ggt gct aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac 147

Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn

35

40

45

cag ttc aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag 195

Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln

50

55

60

aat cag aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc 243

Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser

65

70

75

ttc tgg atc cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac 291

Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr

80

85

90

atc cac aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt 339

Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly

95

100

105

110

tgg aag atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat 387

Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp

115

120

125

atc aac ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa 435

Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu

130

135

140

gac atc tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat 483

Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn

145

150

155

aac ctg aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat 531

Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn

160

165

170

acc gac atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc 579

Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile

175

180

185

190

ttc aaa ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa 627

Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys

195

200

205

tac ttc tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa 675

Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu
 210 215 220

cgg tac aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt 723
 Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly
 225 230 235

aat ccg ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac 771
 Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn
 240 245 250

aag aac tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc 819
 Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile
 255 260 265 270

ctg act cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc 867
 Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg
 275 280 285

gac ctg tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct 915
 Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser
 290 295 300

cag tcc atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg 963
 Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu
 305 310 315

gac ttc ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac 1011
 Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr
 320 325 330

ttc aag aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc 1059
 Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser
 335 340 345 350

gac gaa ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg 1107
 Asp Glu Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro
 355 360 365

acc tac tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac 1155
 Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp
 370 375 380

gaa atc ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta 1203
 Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val
 385 390 395

ttc gaa gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag 1251
 Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys
 400 405 410

gaa gtt aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag 1299
 Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln
 415 420 425 430

ttc atc ccg aaa gac gaa ggt tgg acc gaa tagtaagaat tc 1341
 Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu

Q'

<210> 8

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTB Hc

<400> 8

Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1 5 10 15
 Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
 20 25 30
 Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
 35 40 45
 Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
 50 55 60
 Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
 65 70 75 80
 Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
 85 90 95
 Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
 100 105 110
 Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn
 115 120 125
 Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
 130 135 140
 Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
 145 150 155 160
 Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
 165 170 175
 Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
 180 185 190
 Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
 195 200 205
 Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
 210 215 220
 Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
 225 230 235 240
 Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn
 245 250 255
 Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr
 260 265 270
 Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu
 275 280 285
 Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser
 290 295 300
 Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe
 305 310 315 320
 Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys
 325 330 335
 Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
 340 345 350

Leu	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp	Glu	Gln	Pro	Thr	Tyr
		355					360				365				
Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu	Ser	Thr	Asp	Glu	Ile
	370					375					380				
Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	Ser	Gly	Ile	Val	Phe	Glu
385					390				395						400
Glu	Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	Trp	Tyr	Leu	Lys	Glu	Val
			405					410					415		
Lys	Arg	Lys	Pro	Tyr	Asn	Leu	Lys	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile
			420					425					430		
Pro	Lys	Asp	Glu	Gly	Trp	Thr	Glu								
		435					440								

<210> 9

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (10)...(1359)

<400> 9

gaattcacg	atg	acc	atc	cca	ttc	aac	atc	ttc	tcc	tac	acc	aac	aac	tcc	51	
Met	Thr	Ile	Pro	Phe	Asn	Ile	Phe	Ser	Tyr	Thr	Asn	Asn	Ser			
1					5				10							
ctg	ttg	aag	gac	atc	atc	aac	gag	tac	ttc	aac	aac	atc	aac	gac	tcc	99
Leu	Leu	Lys	Asp	Ile	Ile	Asn	Glu	Tyr	Phe	Asn	Asn	Ile	Asn	Asp	Ser	
15					20				25					30		
aag	atc	ctg	tcc	ctg	cag	aac	cgt	aag	aac	acc	ttg	gtc	gac	acc	tcc	147
Lys	Ile	Leu	Ser	Leu	Gln	Asn	Arg	Lys	Asn	Thr	Leu	Val	Asp	Thr	Ser	
				35				40					45			
ggt	tac	aac	gcc	gag	gtc	tcc	gag	gag	ggt	gac	gtc	cag	ctg	aac	cca	195
Gly	Tyr	Asn	Ala	Glu	Val	Ser	Glu	Glu	Gly	Asp	Val	Gln	Leu	Asn	Pro	
			50				55				60					
atc	ttc	cca	ttc	gac	ttc	aag	ctg	ggt	tcc	tcc	ggt	gag	gac	aga	ggt	243
Ile	Phe	Pro	Phe	Asp	Phe	Lys	Leu	Gly	Ser	Ser	Gly	Glu	Asp	Arg	Gly	
		65					70				75					
aag	gtc	atc	gtc	acc	cag	aac	gag	aac	atc	gtc	tac	aac	tcc	atg	tac	291
Lys	Val	Ile	Val	Thr	Gln	Asn	Glu	Asn	Ile	Val	Tyr	Asn	Ser	Met	Tyr	
	80					85				90						
gag	tcc	ttc	tcc	atc	tcc	ttc	tgg	atc	aga	atc	aac	aag	tgg	gtc	tcc	339
Glu	Ser	Phe	Ser	Ile	Ser	Phe	Trp	Ile	Arg	Ile	Asn	Lys	Trp	Val	Ser	
95					100				105					110		
aac	ttg	cca	ggt	tac	acc	atc	atc	gac	tcc	gtc	aag	aac	aac	tcc	ggt	387
Asn	Leu	Pro	Gly	Tyr	Thr	Ile	Ile	Asp	Ser	Val	Lys	Asn	Asn	Ser	Gly	
			115					120						125		

tgg tcc atc ggt atc atc tcc aac ttc ctg gtc ttc acc ctg aag cag 435
 Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln
 130 135 140

aac gag gac tcc gag cag tcc atc aac ttc tcc tac gac atc tcc aac 483
 Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn
 145 150 155

aac gct cct ggt tac aac aag tgg ttc ttc gtc acc gtc acc aac aac 531
 Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn
 160 165 170

atg atg ggt aac atg aag atc tac atc aac ggt aag ctg atc gac acc 579
 Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr
 175 180 185 190

atc aag gtc aag gag ttg acc ggt atc aac ttc tcc aag acc atc acc 627
 Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr
 195 200 205

ttc gag atc aac aag atc cca gac acc ggt ctg atc acc tcc gac tcc 675
 Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser
 210 215 220

gac aac atc aac atg tgg atc cgt gac ttc tac atc ttc gcc aag gag 723
 Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu
 225 230 235

ttg gac ggt aag gac atc aac atc ctg ttc aac tcc ttg cag tac acc 771
 Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr
 240 245 250

aac gtc gtc aag gac tac tgg ggt aac gac ctg aga tac aac aag gag 819
 Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu
 255 260 265 270

tac tac atg gtc aac atc gac tac ttg aac aga tac atg tac gcc aac 867
 Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn
 275 280 285

tcc aga cag atc gtc ttc aac acc aga cgt aac aac aac gac ttc aac 915
 Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn
 290 295 300

gag ggt tac aag atc atc atc aag cgt atc aga ggt aac acc aac gac 963
 Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp
 305 310 315

acc aga gtc aga ggt ggt gac atc ctg tac ttc gac atg act atc aac 1011
 Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn
 320 325 330

aac aag gcc tac aac ctg ttc atg aag aac gag acc atg tac gcc gac 1059
 Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp
 335 340 345 350

aac cac tcc acc gag gac atc tac gcc atc ggt ctg cgt gag cag acc 1107
 Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr
 355 360 365

 aag gac atc aac gac aac atc atc ttc cag atc cag cca atg aac aac 1155
 Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn
 370 375 380

 act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag 1203
 Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu
 385 390 395

 aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt 1251
 Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly
 400 405 410

 ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt 1299
 Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly
 415 420 425 430

 aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc 1347
 Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val
 435 440 445

 cca gtc tcc gag taataggaat tc 1371
 Pro Val Ser Glu
 450

<210> 10

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTC Hc

<400> 10

Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu
 1 5 10 15
 Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile
 20 25 30
 Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr
 35 40 45
 Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe
 50 55 60
 Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
 65 70 75 80
 Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser
 85 90 95
 Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu
 100 105 110
 Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser
 115 120 125
 Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu
 130 135 140

Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala
 145 150 155 160
 Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met
 165 170 175
 Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys
 180 185 190
 Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu
 195 200 205
 Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn
 210 215 220
 Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp
 225 230 235 240
 Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val
 245 250 255
 Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
 260 265 270
 Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg
 275 280 285
 Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly
 290 295 300
 Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg
 305 310 315 320
 Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys
 325 330 335
 Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His
 340 345 350
 Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp
 355 360 365
 Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr
 370 375 380
 Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile
 385 390 395 400
 Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp
 405 410 415
 Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr
 420 425 430
 Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val
 435 440 445
 Ser Glu
 450

<210> 11

<211> 1374

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (10)...(1362)

<400> 11

gaattcacg atg cgt ttg aag gct aag gtc aac gag tcc ttc gag aac acc 51
 Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr

1

5

10

atg cca ttc aac atc ttc tcc tac acc aac aac tcc ttg ttg aag gac	99
Met Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp	
15 20 25 30	
atc atc aac gag tac ttc aac tcc atc aac gac tcc aag atc ttg tcc	147
Ile Ile Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser	
35 40 45	
ttg cag aac aag aag aac gcc ttg gtc gac acc tcc ggt tac aac gcc	195
Leu Gln Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala	
50 55 60	
gag gtc aga gtc ggt gac aac gtc cag ttg aac acc atc tac acc aac	243
Glu Val Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn	
65 70 75	
gac ttc aag ttg tcc tct tcc ggt gac aag atc atc gtc aac ttg aac	291
Asp Phe Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn	
80 85 90	
aac aac atc ttg tac tcc gcc atc tac gag aac tcc tct gtc tcc ttc	339
Asn Asn Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe	
95 100 105 110	
tggt atc aag atc tcc aag gac ttg acc aac tcc cac aac gag tac acc	387
Trp Ile Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr	
115 120 125	
atc atc aac tcc atc gag cag aac tcc ggt tgg aag ttg tgt atc cgt	435
Ile Ile Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg	
130 135 140	
aac ggt aac atc gag tgg atc ttg cag gac gtc aac cgt aag tac aag	483
Asn Gly Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys	
145 150 155	
tcc ttg atc ttc gac tac tcc gag tcc ttg tcc cac acc ggt tac acc	531
Ser Leu Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr	
160 165 170	
aac aag tgg ttc ttc gtc acc atc acc aac aac atc atg ggt tac atg	579
Asn Lys Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met	
175 180 185 190	
aag ttg tac atc aac ggt gag ttg aag cag tcc cag aag atc gag gac	627
Lys Leu Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp	
195 200 205	
ctg gac gag gtc aag ctg gac aag acc atc gtc ttc ggt atc gac gag	675
Leu Asp Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu	
210 215 220	
aac atc gac gag aac cag atg ttg tgg atc cgt gac ttc aac atc ttc	723
Asn Ile Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe	
225 230 235	

tcc aag gag ctg tcc aac gag gac atc aac atc gtc tac gag ggt cag 771
Ser Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln
240 245 250

atc ctg agg aac gtc atc aag gac tac tgg ggt aac cca ctg aag ttc 819
Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe
255 260 265 270

gac acc gag tac tac atc atc aac gac aac tac atc gac cgt tac atc 867
Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile
275 280 285

gcc cca gag tcc aac gtc ctg gtc ctg gtc cag tac cct gac cgt tcc 915
Ala Pro Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Arg Ser
290 295 300

aag ctg tac acc ggt aac cct atc acc atc aag tcc gtc tcc gac aag 963
Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys
305 310 315

aac cct tac tcc cgt atc ctg aac ggt gac aac atc atc ctg cac atg 1011
Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met
320 325 330

ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc 1059
Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile
335 340 345 350

tac gcc acc cag ggt ggt gac tgt tcc cag aac tgt gtc tac gcc ctg 1107
Tyr Ala Thr Gln Gly Gly Asp Cys Ser Gln Asn Cys Val Tyr Ala Leu
355 360 365

aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc 1155
Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile
370 375 380

aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc 1203
Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser
385 390 395

ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt 1251
Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg
400 405 410

ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag 1299
Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu
415 420 425 430

acc aag ctg ctg tcc acc tcc tcc ttc tgg aag ttc atc tcc cgt gac 1347
Thr Lys Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp
435 440 445

cca ggt tgg gtc gag taataggaat tc 1374
Pro Gly Trp Val Glu
450

<210> 12
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hc

<400> 12
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
1 5 10 15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
20 25 30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
35 40 45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
50 55 60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65 70 75 80
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
85 90 95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
100 105 110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
115 120 125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
130 135 140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145 150 155 160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
165 170 175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
180 185 190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
195 200 205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
210 215 220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys
225 230 235 240
Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu
245 250 255
Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr
260 265 270
Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro
275 280 285
Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Arg Ser Lys Leu
290 295 300
Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro
305 310 315 320
Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr
325 330 335
Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala
340 345 350
Thr Gln Gly Gly Asp Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu
355 360 365
Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn

370		375		380
Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg				
385		390		400
Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser				
	405		410	415
Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys				
	420		425	430
Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly				
	435		440	445
Trp Val Glu				
450				

<210> 13
 <211> 1400
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (10)...(1356)

<400> 13
 gaattcacc atg gga gag agt cag caa gaa cta aat tct atg gta act gat 51
 Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp
 1 5 10

acc cta aat aat agt att cct ttt aag ctt tct tct tat aca gat gat 99
 Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp
 15 20 25 30

aaa att tta att tcc tac ttc aac aag ttc ttc aag aga att aag tct 147
 Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
 35 40 45

tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc gac act 195
 Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
 50 55 60

tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac aag tac 243
 Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
 65 70 75

cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt act gag 291
 Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu
 80 85 90

ctg aac atc tct caa aac gac tac att atc tac gac aac aag tac aag 339
 Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
 95 100 105 110

aac ttc tct att tct ttc tgg gtc agg att cct aac tac gac aac aag 387
 Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
 115 120 125

atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg aga gac 435
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
130 135 140

aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atc att tgg 483
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
145 150 155

acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc aac tac 531
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr
160 165 170

ggg aac gca aac ggt att tct gac tac atc aac aag tgg att ttc gtc 579
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val
175 180 185 190

act atc act aac gac aga tta ggt gac tct aag ctt tac att aac ggt 627
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly
195 200 205

aac tta atc gac caa aag tcc att tta aac tta ggt aac att cac gtt 675
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val
210 215 220

tct gac aac atc tta ttc aag atc gtt aac tgc agt tac acc aga tac 723
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr
225 230 235

att ggc att aga tac ttc aac att ttc gac aag gag tta gac gag acc 771
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr
240 245 250

gag att caa act tta tac agc aac gaa cct aac acc aat att ttg aag 819
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys
255 260 265 270

gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac tta tta 867
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu
275 280 285

aac gtg tta aag cca aac aac ttc att gat agg aga aag gat tct act 915
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr
290 295 300

tta agc att aac aac atc aga agc act att ctt tta gct aac aga tta 963
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu
305 310 315

tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct tct act 1011
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr
320 325 330

aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac ttc gtc 1059
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val
335 340 345 350

gct agc aag act cac tta ttc cca tta tat gct gat acc gct acc acc 1107

Ala	Ser	Lys	Thr	His	Leu	Phe	Pro	Leu	Tyr	Ala	Asp	Thr	Ala	Thr	Thr		
				355					360					365			
aac	aag	gag	aag	acc	atc	aag	atc	tcc	tcc	tct	ggc	aac	aga	ttt	aac	1155	
Asn	Lys	Glu	Lys	Thr	Ile	Lys	Ile	Ser	Ser	Ser	Gly	Asn	Arg	Phe	Asn		
			370					375					380				
caa	gtc	gtc	gtt	atg	aac	tcc	gtc	ggg	aac	aac	tgt	acc	atg	aac	ttt	1203	
Gln	Val	Val	Val	Met	Asn	Ser	Val	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe		
			385				390					395					
aaa	aat	aat	aat	gga	aat	aat	att	ggg	ttg	tta	ggg	ttc	aag	gca	gat	1251	
Lys	Asn	Asn	Asn	Gly	Asn	Asn	Ile	Gly	Leu	Leu	Gly	Phe	Lys	Ala	Asp		
	400					405					410						
act	gta	gtt	gct	agt	act	tgg	tat	tat	acc	cac	atg	aga	gat	cac	acc	1299	
Thr	Val	Val	Ala	Ser	Thr	Trp	Tyr	Tyr	Thr	His	Met	Arg	Asp	His	Thr		
415					420				425						430		
aac	agc	aat	gga	tgt	ttt	tgg	aac	ttt	att	tct	gaa	gaa	cat	gga	tgg	1347	
Asn	Ser	Asn	Gly	Cys	Phe	Trp	Asn	Phe	Ile	Ser	Glu	Glu	His	Gly	Trp		
				435				440						445			
caa	gaa	aaa	taatagggat	ccgcggccgc	acgcgtcccg	ggactagtga										1396	
Gln	Glu	Lys															

attc 1400

<210> 14

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTE Hc

<400> 14

Met	Gly	Glu	Ser	Gln	Gln	Glu	Leu	Asn	Ser	Met	Val	Thr	Asp	Thr	Leu		
1				5				10						15			
Asn	Asn	Ser	Ile	Pro	Phe	Lys	Leu	Ser	Ser	Tyr	Thr	Asp	Asp	Lys	Ile		
			20					25					30				
Leu	Ile	Ser	Tyr	Phe	Asn	Lys	Phe	Phe	Lys	Arg	Ile	Lys	Ser	Ser	Ser		
		35				40						45					
Val	Leu	Asn	Met	Arg	Tyr	Lys	Asn	Asp	Lys	Tyr	Val	Asp	Thr	Ser	Gly		
	50					55					60						
Tyr	Asp	Ser	Asn	Ile	Asn	Ile	Asn	Gly	Asp	Val	Tyr	Lys	Tyr	Pro	Thr		
65				70				75						80			
Asn	Lys	Asn	Gln	Phe	Gly	Ile	Tyr	Asn	Asp	Lys	Leu	Thr	Glu	Leu	Asn		
			85					90						95			
Ile	Ser	Gln	Asn	Asp	Tyr	Ile	Ile	Tyr	Asp	Asn	Lys	Tyr	Lys	Asn	Phe		
		100						105					110				
Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile	Pro	Asn	Tyr	Asp	Asn	Lys	Ile	Val		
		115					120					125					
Asn	Val	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Arg	Asp	Asn	Asn		
	130					135					140						

Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
 145 150 155 160
 Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
 165 170 175
 Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
 180 185 190
 Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
 195 200 205
 Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
 210 215 220
 Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
 225 230 235 240
 Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
 245 250 255
 Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
 260 265 270
 Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
 275 280 285
 Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
 290 295 300
 Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser
 305 310 315 320
 Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp
 325 330 335
 Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser
 340 345 350
 Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys
 355 360 365
 Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val
 370 375 380
 Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn
 385 390 395 400
 Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val
 405 410 415
 Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn Ser
 420 425 430
 Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu
 435 440 445
 Lys

<210> 15
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BONTA Hc

<221> CDS
 <222> (10)...(1305)

<400> 15
 gaattcacg atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51
 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
 1 5 10

aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac	99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr	
15 20 25 30	
gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc	147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser	
35 40 45	
atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga	195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly	
50 55 60	
atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac	243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp	
65 70 75	
atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc	291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val	
80 85 90	
cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc	339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr	
95 100 105 110	
atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg	387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu	
115 120 125	
aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat	435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn	
130 135 140	
cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac	483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr	
145 150 155	
atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac	531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn	
160 165 170	
tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc	579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser	
175 180 185 190	
aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc	627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val	
195 200 205	
ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc	675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe	
210 215 220	
gac act gag ttg ggt aag acc gag atc gag acc ttg tac tcc gac gag	723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu	
225 230 235	

Q

cct gac cca tcc atc ctg aag gac ttc tgg ggt aac tac ctg ctg tac 771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
240 245 250

aac aaa cgt tac tac ttg ctg aac ttg ttg cgt acc gac aag tcc atc 819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
255 260 265 270

acc cag aac tcc aac ttc ttg aac atc aac cag cag aga ggt gtc tac 867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
275 280 285

cag aag cca aac atc ttc tcc aac acc aga ttg tac acc gga gtc gag 915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
290 295 300

gtc att atc aga aag aac gga tct act gat att tcc aac acc gat aac 963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
305 310 315

ttc gtc aga aag aac gat ctg gct tac atc aac gtt gtc gac aga gat 1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
320 325 330

gtc gaa tac cgt ctg tac gcc gat atc tct atc gcc aaa cct gaa aag 1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
335 340 345 350

atc atc aag ctg atc cgt acc tct aac tct aac aac tct ctg gga caa 1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
355 360 365

atc atc gtc atg gac tcc atc ggt aat aac tgt acc atg aac ttc cag 1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
370 375 380

aac aac aac ggt gga aac atc ggt ttg ttg ggt ttc cac tcc aac aac 1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
385 390 395

ttg gtc gct tcc tcc tgg tac tac aac aac atc cgt aag aac acc tcc 1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
400 405 410

tcc aac ggt tgc ttc tgg tcc ttc atc tcc aag gag cac ggt tgg cag 1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
415 420 425 430

gag aac taataggaat tc 1317
Glu Asn

<210> 16
<211> 432
<212> PRT
<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hc

<400> 16

Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
1 5 10 15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
20 25 30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
35 40 45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
50 55 60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65 70 75 80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
85 90 95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
100 105 110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
115 120 125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
130 135 140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145 150 155 160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
165 170 175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
180 185 190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
195 200 205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
210 215 220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225 230 235 240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
245 250 255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
260 265 270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
275 280 285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
290 295 300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305 310 315 320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
325 330 335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
340 345 350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
355 360 365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
370 375 380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385 390 395 400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn

				405						410					415			
Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln	Glu	Asn			
			420					425					430					

<210> 17
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (10)...(1356)

<400> 17
 gaattcacg atg aag gac acc atc ctg atc cag gtc ttc aac aac tac atc 51
 Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile
 1 5 10

tcc aac atc tcc tcc aac gcc atc ctg tcc ctg tcc tac cgt ggt ggt 99
 Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly
 15 20 25 30

cgt ctg atc gac tcc tcc ggt tac gga gcc acc atg aac gtc ggt tcc 147
 Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser
 35 40 45

gac gtc atc ttc aac gac atc ggt aac ggt cag ttc aag ctg aac aac 195
 Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn
 50 55 60

tcc gag aac tcc aac atc acc gcc cac cag tcc aag ttc gtc gtc tac 243
 Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr
 65 70 75

gac tcc atg ttc gac aac ttc tcc atc aac ttc tgg gtc cgt acc cca 291
 Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro
 80 85 90

aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc 339
 Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr
 95 100 105 110

atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag 387
 Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys
 115 120 125

gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag 435
 Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys
 130 135 140

tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc 483
 Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile
 145 150 155

aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc 531
 Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala
 160 165 170

aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac 579
 Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn
 175 180 185 190

ctg gac cgt atc aac tcc tcc aac gac atc gac ttc aag ctg atc aac 627
 Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn
 195 200 205

tgt acc gac acc acc aag ttc gtc tgg atc aag gac ttc aac atc ttc 675
 Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe
 210 215 220

ggt cgt gag ctg aac gcc acc gag gtc tcc tcc ctg tac tgg atc cag 723
 Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln
 225 230 235

tcc tcc acc aac acc ctg aag gac ttc tgg gga aac cca ctg cgt tac 771
 Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr
 240 245 250

gac acc cag tac tac ctg ttc aac cag ggt atg cag aac atc tac atc 819
 Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile
 255 260 265 270

aag tac ttc tcc aag gcc tcc atg ggt gag acc gcc cct cgt acc aac 867
 Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn
 275 280 285

ttc aac aac gcc gcc atc aac tac cag aac ctg tac ctg ggt ctg cgt 915
 Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg
 290 295 300

ttc atc atc aag aag gcc tcc aac tcc cgt aac atc aac aac gac aac 963
 Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn
 305 310 315

atc gtc cgt gag ggt gac tac atc tac ctg aac atc gac aac atc tcc 1011
 Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser
 320 325 330

gac gag tcc tac cgt gtc tac gtc ctg gtc aac tcc aag gag atc cag 1059
 Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln
 335 340 345 350

acc cag ctg ttc ctg gcc cca atc aac gac gac cct acc ttc tac gac 1107
 Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp
 355 360 365

gtc ctg cag atc aag aag tac tac gag aag acc acc tac aac tgt cag 1155
 Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln
 370 375 380

atc ctg tgc gag aag gac acc aag acc ttc gga ctg ttc ggt atc ggt 1203

Ile	Leu	Cys	Glu	Lys	Asp	Thr	Lys	Thr	Phe	Gly	Leu	Phe	Gly	Ile	Gly		
		385						390					395				
aag	ttc	gtc	aag	gac	tac	ggg	tac	gtc	tgg	gac	acc	tac	gac	aac	tac	1251	
Lys	Phe	Val	Lys	Asp	Tyr	Gly	Tyr	Val	Trp	Asp	Thr	Tyr	Asp	Asn	Tyr		
	400					405					410						
ttc	tgt	atc	tcc	cag	tgg	tac	ctg	cgt	cgt	atc	tcc	gag	aac	atc	aac	1299	
Phe	Cys	Ile	Ser	Gln	Trp	Tyr	Leu	Arg	Arg	Ile	Ser	Glu	Asn	Ile	Asn		
415					420					425					430		
aag	ctg	cgt	ctg	gga	tgt	aac	tgg	cag	ttc	atc	cca	gtc	gac	gag	ggg	1347	
Lys	Leu	Arg	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	Pro	Val	Asp	Glu	Gly		
				435					440						445		
tg	g	a	g	a	a	a	a	a	a	a	a	a	a	a	a	1368	
Trp	Thr	Glu															

<210> 18
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTG Hc

<400> 18

Met	Lys	Asp	Thr	Ile	Leu	Ile	Gln	Val	Phe	Asn	Asn	Tyr	Ile	Ser	Asn
1				5					10					15	
Ile	Ser	Ser	Asn	Ala	Ile	Leu	Ser	Leu	Ser	Tyr	Arg	Gly	Gly	Arg	Leu
			20					25					30		
Ile	Asp	Ser	Ser	Gly	Tyr	Gly	Ala	Thr	Met	Asn	Val	Gly	Ser	Asp	Val
			35				40					45			
Ile	Phe	Asn	Asp	Ile	Gly	Asn	Gly	Gln	Phe	Lys	Leu	Asn	Asn	Ser	Glu
	50					55					60				
Asn	Ser	Asn	Ile	Thr	Ala	His	Gln	Ser	Lys	Phe	Val	Val	Tyr	Asp	Ser
65				70					75					80	
Met	Phe	Asp	Asn	Phe	Ser	Ile	Asn	Phe	Trp	Val	Arg	Thr	Pro	Lys	Tyr
			85					90						95	
Asn	Asn	Asn	Asp	Ile	Gln	Thr	Tyr	Leu	Gln	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105					110		
Ser	Cys	Ile	Lys	Asn	Asp	Ser	Gly	Trp	Lys	Val	Ser	Ile	Lys	Gly	Asn
			115				120					125			
Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Val	Asn	Ala	Lys	Ser	Lys	Ser	Ile
	130					135				140					
Phe	Phe	Glu	Tyr	Ser	Ile	Lys	Asp	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Lys
145					150				155					160	
Trp	Phe	Ser	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Gly	Asn	Ala	Asn	Ile
			165					170						175	
Tyr	Ile	Asn	Gly	Ser	Leu	Lys	Lys	Ser	Glu	Lys	Ile	Leu	Asn	Leu	Asp
			180					185					190		
Arg	Ile	Asn	Ser	Ser	Asn	Asp	Ile	Asp	Phe	Lys	Leu	Ile	Asn	Cys	Thr
			195				200					205			
Asp	Thr	Thr	Lys	Phe	Val	Trp	Ile	Lys	Asp	Phe	Asn	Ile	Phe	Gly	Arg

210 215 220
 Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser
 225 230 235 240
 Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
 245 250 255
 Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr
 260 265 270
 Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn
 275 280 285
 Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile
 290 295 300
 Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
 305 310 315
 Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
 325 330 335
 Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln
 340 345 350
 Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu
 355 360 365
 Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu
 370 375 380
 Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe
 385 390 395 400
 Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys
 405 410 415
 Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu
 420 425 430
 Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr
 435 440 445
 Glu

<210> 19
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (1)...(1239)

<400> 19
 atg gct ctg aac gac ctg tgc atc aaa gtt aac aac tgg gac ctg ttc 48
 Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1 5 10 15

 ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa 96
 Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
 20 25 30

 gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct 144
 Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
 35 40 45

ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa 192
 Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
 50 55 60

ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag 240
 Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
 65 70 75 80

ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac 288
 Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
 85 90 95

gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc 336
 Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
 100 105 110

gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct 384
 Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
 115 120 125

ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt 432
 Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
 130 135 140

aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt 480
 Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
 145 150 155 160

gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc 528
 Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
 165 170 175

act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg 576
 Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
 180 185 190

gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct 624
 Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
 195 200 205

ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc 672
 Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
 210 215 220

gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac 720
 Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
 225 230 235 240

aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac 768
 Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
 245 250 255

gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct 816
 Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
 260 265 270

aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct 864

Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala		
		275					280					285					
ctg	gaa	aac	cag	gct	gaa	gct	act	aaa	gct	atc	atc	aac	tac	cag	tac	912	
Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr		
		290					295				300						
aac	cag	tac	acc	gaa	gaa	gaa	aag	aac	aac	atc	aac	ttc	aac	atc	gat	960	
Asn	Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp		
305					310					315					320		
gac	ctg	tcc	tct	aaa	ctg	aac	gaa	tcc	atc	aac	aaa	gct	atg	atc	aac	1008	
Asp	Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn		
				325					330					335			
atc	aac	aaa	ttc	ctg	aac	cag	tgc	tct	gtt	tcc	tac	ctg	atg	aac	tct	1056	
Ile	Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser		
			340					345					350				
atg	atc	ccg	tac	ggc	gtt	aaa	cgc	ctg	gaa	gac	ttc	gac	gct	tcc	ctg	1104	
Met	Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu		
		355					360				365						
aaa	gac	gct	ctg	ctg	aaa	tac	atc	cgt	gac	aac	tac	ggc	act	ctg	atc	1152	
Lys	Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Arg	Asp	Asn	Tyr	Gly	Thr	Leu	Ile		
	370					375					380						
ggc	cag	gtt	gac	cgt	ctg	aaa	gac	aag	gtt	aac	aac	acc	ctg	tct	act	1200	
Gly	Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr		
	385				390				395						400		
gac	atc	ccg	ttc	cag	ctg	tcc	aaa	tac	gtt	gac	aac	cag	taa			1242	
Asp	Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln					
				405					410								

<210> 20

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hn

<400> 20

Met	Ala	Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe		
1			5						10					15			
Phe	Ser	Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu		
			20					25					30				
Glu	Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser		
		35				40						45					
Leu	Asp	Leu	Ile	Gln	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu		
	50					55				60							
Pro	Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln		
	65				70				75					80			
Leu	Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr		

85 90 95
 Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
 100 105 110
 Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
 115 120 125
 Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
 130 135 140
 Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
 145 150 155 160
 Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
 165 170 175
 Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
 180 185 190
 Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
 195 200 205
 Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
 210 215 220
 Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
 225 230 235 240
 Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
 245 250 255
 Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
 260 265 270
 Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
 275 280 285
 Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
 290 295 300
 Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
 305 310 315 320
 Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
 325 330 335
 Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
 340 345 350
 Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
 355 360 365
 Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
 370 375 380
 Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
 385 390 395 400
 Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
 405 410

<210> 21
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BONTA Hc

<221> CDS
 <222> (1)...(1239)

<400> 21
 atg gct cca gga atc tgt atc gac gtc gac aac gag gac ttg ttc ttc 48
 Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe

1	5	10	15	
atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga	96			
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg				
20 25 30				
atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc	144			
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile				
35 40 45				
aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca	192			
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro				
50 55 60				
tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc	240			
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val				
65 70 75 80				
tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc	288			
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr				
85 90 95				
atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac	336			
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp				
100 105 110				
atc tcc ttg acc tct tcc ttc gac gac gcc ctg ctg ttc tcc aac aag	384			
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys				
115 120 125				
gtc tac tcc ttc ttc tcc atg gac tac atc aag act gct aac aag gtc	432			
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val				
130 135 140				
gtc gag gcc ggt ttg ttc gct ggt tgg gtc aag cag atc gtc aac gat	480			
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp				
145 150 155 160				
ttc gtc atc gag gct aac aag tcc aac acc atg gac aag att gcc gac	528			
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp				
165 170 175				
atc tcc ttg att gtc cca tac atc ggt ttg gcc ttg aac gtc ggt aac	576			
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn				
180 185 190				
gag acc gcc aag ggt aac ttc gag aac gct ttc gag atc gct ggt gcc	624			
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala				
195 200 205				
tcc atc ttg ttg gag ttc atc cca gag ttg ttg atc cca gtc gtc ggt	672			
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly				
210 215 220				
gcc ttc ttg ttg gag tcc tac atc gac aac aag aac aag atc atc aag	720			
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys				
225 230 235 240				

Q

acc atc gac aac gct ttg acc aag aga aac gag aag tgg tcc gac atg 768
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
245 250 255

tac ggt ttg atc gtc gcc caa tgg ttg tcc acc gtc aac acc caa ttc 816
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
260 265 270

tac acc atc aag gag ggt atg tac aag gcc ttg aac tac cag gcc caa 864
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
275 280 285

gct ttg gag gag atc atc aag tac aga tac aac atc tac tcc gag aag 912
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
290 295 300

gag aag tcc aac att aac atc gac ttc aac gac atc aac tcc aag ctg 960
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
305 310 315 320

aac gag ggt att aac cag gcc atc gac aac atc aac aac ttc atc aac 1008
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
325 330 335

ggt tgt tcc gtc tcc tac ttg atg aag aag atg att cca ttg gcc gtc 1056
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
340 345 350

gag aag ttg ttg gac ttc gac aac acc ctg aag aag aac ttg ttg aac 1104
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn
355 360 365

tac atc gac gag aac aag ttg tac ttg atc ggt tcc gct gag tac gag 1152
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
370 375 380

aag tcc aag gtc aac aag tac ttg aag acc atc atg cca ttc gac ttg 1200
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
385 390 395 400

tcc atc tac acc aac gac acc atc ttg atc gag atg ttc taa 1242
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
405 410

<210> 22
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTB Hn

<400> 22
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe

1				5					10					15			
Ile	Ala	Asp	Lys	Asn	Ser	Phe	Ser	Asp	Asp	Leu	Ser	Lys	Asn	Glu	Arg		
			20					25					30				
Ile	Glu	Tyr	Asn	Thr	Gln	Ser	Asn	Tyr	Ile	Glu	Asn	Asp	Phe	Pro	Ile		
		35					40					45					
Asn	Glu	Leu	Ile	Leu	Asp	Thr	Asp	Leu	Ile	Ser	Lys	Ile	Glu	Leu	Pro		
		50				55					60						
Ser	Glu	Asn	Thr	Glu	Ser	Leu	Thr	Asp	Phe	Asn	Val	Asp	Val	Pro	Val		
65					70					75				80			
Tyr	Glu	Lys	Gln	Pro	Ala	Ile	Lys	Lys	Ile	Phe	Thr	Asp	Glu	Asn	Thr		
			85						90					95			
Ile	Phe	Gln	Tyr	Leu	Tyr	Ser	Gln	Thr	Phe	Pro	Leu	Asp	Ile	Arg	Asp		
		100					105						110				
Ile	Ser	Leu	Thr	Ser	Ser	Phe	Asp	Asp	Ala	Leu	Leu	Phe	Ser	Asn	Lys		
		115				120						125					
Val	Tyr	Ser	Phe	Phe	Ser	Met	Asp	Tyr	Ile	Lys	Thr	Ala	Asn	Lys	Val		
		130				135					140						
Val	Glu	Ala	Gly	Leu	Phe	Ala	Gly	Trp	Val	Lys	Gln	Ile	Val	Asn	Asp		
145					150					155				160			
Phe	Val	Ile	Glu	Ala	Asn	Lys	Ser	Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp		
			165					170					175				
Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn		
		180					185					190					
Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu	Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala		
		195				200					205						
Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Leu	Leu	Ile	Pro	Val	Val	Gly		
		210				215					220						
Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile	Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys		
225					230					235				240			
Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys	Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met		
			245						250					255			
Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp	Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe		
		260					265					270					
Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr	Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln		
		275				280					285						
Ala	Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys		
		290				295				300							
Glu	Lys	Ser	Asn	Ile	Asn	Ile	Asp	Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu		
305					310					315				320			
Asn	Glu	Gly	Ile	Asn	Gln	Ala	Ile	Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn		
			325					330					335				
Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val		
		340					345				350						
Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn		
		355				360					365						
Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu		
		370				375				380							
Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu		
385					390					395				400			
Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe					
			405					410									

<210> 23
 <211> 1200
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<221> CDS

<222> (1)...(1197)

<400> 23

atg tcc ctg tac aac aag acc ctt gac tgt aga gag ctg ctg gtg aag 48
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
1 5 10 15

aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac 96
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
20 25 30

atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac 144
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
35 40 45

cca gac aac gtg tca gta gac caa gtg atc ctc agt aag aac acc tcc 192
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
50 55 60

gag cat gga caa cta gac ctg ctc tac cct agt atc gac agt gag agt 240
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
65 70 75 80

gag atc ctg cca ggg gag aat caa gtc ttc tac gac aac cgt acc cag 288
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
85 90 95

aac gtg gac tac ctg aac tcc tac tac tac cta gag tct cag aag ctg 336
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
100 105 110

agt gac aac gtg gag gac ttc act ttc acg cgt tca atc gag gag gct 384
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
115 120 125

ctg gac aac agt gca aag gtg tac act tac ttc cct acc ctg gct aac 432
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
130 135 140

aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac 480
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145 150 155 160

gac gtg gtt gag gac ttc act acc aac atc ctg cgt aag gac aca ctg 528
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
165 170 175

gac aag atc tca gat gtg tca gct atc atc ccc tac atc gga ccc gca 576
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
180 185 190

ctg aac atc tcc aac tct gtg cgt cgt gga aac ttc act gag gca ttc 624

Leu	Asn	Ile	Ser	Asn	Ser	Val	Arg	Arg	Gly	Asn	Phe	Thr	Glu	Ala	Phe		
	195						200					205					
gca	gtc	act	ggg	gtc	acc	atc	ctg	ctg	gag	gca	ttc	cct	gag	ttc	aca	672	
Ala	Val	Thr	Gly	Val	Thr	Ile	Leu	Leu	Glu	Ala	Phe	Pro	Glu	Phe	Thr		
	210					215					220						
atc	cct	gct	ctg	ggg	gca	ttc	gtg	atc	tac	agt	aag	gtc	cag	gag	cga	720	
Ile	Pro	Ala	Leu	Gly	Ala	Phe	Val	Ile	Tyr	Ser	Lys	Val	Gln	Glu	Arg		
225					230					235					240		
aac	gag	atc	atc	aag	acc	atc	gac	aac	tgt	ctg	gag	cag	agg	atc	aag	768	
Asn	Glu	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Lys		
				245					250					255			
aga	tgg	aag	gac	tcc	tac	gag	tgg	atg	atg	gga	acg	tgg	ttg	tcc	agg	816	
Arg	Trp	Lys	Asp	Ser	Tyr	Glu	Trp	Met	Met	Gly	Thr	Trp	Leu	Ser	Arg		
			260					265					270				
atc	atc	acc	cag	ttc	aac	aac	atc	tcc	tac	cag	atg	tac	gac	tcc	ctg	864	
Ile	Ile	Thr	Gln	Phe	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Tyr	Asp	Ser	Leu		
		275					280					285					
aac	tac	cag	gca	ggg	gca	atc	aag	gct	aag	atc	gac	ctg	gag	tac	aag	912	
Asn	Tyr	Gln	Ala	Gly	Ala	Ile	Lys	Ala	Lys	Ile	Asp	Leu	Glu	Tyr	Lys		
	290					295					300						
aag	tac	tcc	gga	agc	gac	aag	gag	aac	atc	aag	agc	cag	gtt	gag	aac	960	
Lys	Tyr	Ser	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Lys	Ser	Gln	Val	Glu	Asn		
305					310					315				320			
ctg	aag	aac	agt	ctg	gac	gtc	aag	atc	tcg	gag	gca	atg	aac	aac	atc	1008	
Leu	Lys	Asn	Ser	Leu	Asp	Val	Lys	Ile	Ser	Glu	Ala	Met	Asn	Asn	Ile		
				325					330					335			
aac	aag	ttc	atc	cga	gag	tgc	tcc	gtc	acc	tac	ctg	ttc	aag	aac	atg	1056	
Asn	Lys	Phe	Ile	Arg	Glu	Cys	Ser	Val	Thr	Tyr	Leu	Phe	Lys	Asn	Met		
			340					345					350				
ctg	cct	aag	gtc	atc	gac	gag	ctg	aac	gag	ttc	gac	cga	aac	acc	aag	1104	
Leu	Pro	Lys	Val	Ile	Asp	Glu	Leu	Asn	Glu	Phe	Asp	Arg	Asn	Thr	Lys		
		355					360					365					
gca	aag	ctg	atc	aac	ctg	atc	gac	tcc	cat	aac	atc	atc	ctg	gtc	ggg	1152	
Ala	Lys	Leu	Ile	Asn	Leu	Ile	Asp	Ser	His	Asn	Ile	Ile	Leu	Val	Gly		
	370					375					380						
gag	gtc	gac	aag	ctg	aag	gca	aag	gta	aac	aac	agc	ttc	cag	aac		1197	
Glu	Val	Asp	Lys	Leu	Lys	Ala	Lys	Val	Asn	Asn	Ser	Phe	Gln	Asn			
385					390					395							
taa																	1200

<210> 24

<211> 399


<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTC Hn

<400> 24



Met	Ser	Leu	Tyr	Asn	Lys	Thr	Leu	Asp	Cys	Arg	Glu	Leu	Leu	Val	Lys
1				5					10					15	
Asn	Thr	Asp	Leu	Pro	Phe	Ile	Gly	Asp	Ile	Ser	Asp	Val	Lys	Thr	Asp
			20					25					30		
Ile	Phe	Leu	Arg	Lys	Asp	Ile	Asn	Glu	Glu	Thr	Glu	Val	Ile	Tyr	Tyr
		35					40					45			
Pro	Asp	Asn	Val	Ser	Val	Asp	Gln	Val	Ile	Leu	Ser	Lys	Asn	Thr	Ser
	50					55					60				
Glu	His	Gly	Gln	Leu	Asp	Leu	Leu	Tyr	Pro	Ser	Ile	Asp	Ser	Glu	Ser
65					70					75					80
Glu	Ile	Leu	Pro	Gly	Glu	Asn	Gln	Val	Phe	Tyr	Asp	Asn	Arg	Thr	Gln
				85					90					95	
Asn	Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu
			100					105					110		
Ser	Asp	Asn	Val	Glu	Asp	Phe	Thr	Phe	Thr	Arg	Ser	Ile	Glu	Glu	Ala
			115				120					125			
Leu	Asp	Asn	Ser	Ala	Lys	Val	Tyr	Thr	Tyr	Phe	Pro	Thr	Leu	Ala	Asn
	130					135					140				
Lys	Val	Asn	Ala	Gly	Val	Gln	Gly	Gly	Leu	Phe	Leu	Met	Trp	Ala	Asn
145					150					155					160
Asp	Val	Val	Glu	Asp	Phe	Thr	Thr	Asn	Ile	Leu	Arg	Lys	Asp	Thr	Leu
				165					170					175	
Asp	Lys	Ile	Ser	Asp	Val	Ser	Ala	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala
			180					185					190		
Leu	Asn	Ile	Ser	Asn	Ser	Val	Arg	Arg	Gly	Asn	Phe	Thr	Glu	Ala	Phe
		195					200					205			
Ala	Val	Thr	Gly	Val	Thr	Ile	Leu	Leu	Glu	Ala	Phe	Pro	Glu	Phe	Thr
	210					215					220				
Ile	Pro	Ala	Leu	Gly	Ala	Phe	Val	Ile	Tyr	Ser	Lys	Val	Gln	Glu	Arg
225					230					235					240
Asn	Glu	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Lys
				245					250					255	
Arg	Trp	Lys	Asp	Ser	Tyr	Glu	Trp	Met	Met	Gly	Thr	Trp	Leu	Ser	Arg
			260					265					270		
Ile	Ile	Thr	Gln	Phe	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Tyr	Asp	Ser	Leu
		275					280					285			
Asn	Tyr	Gln	Ala	Gly	Ala	Ile	Lys	Ala	Lys	Ile	Asp	Leu	Glu	Tyr	Lys
	290					295					300				
Lys	Tyr	Ser	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Lys	Ser	Gln	Val	Glu	Asn
305					310					315					320
Leu	Lys	Asn	Ser	Leu	Asp	Val	Lys	Ile	Ser	Glu	Ala	Met	Asn	Asn	Ile
				325					330					335	
Asn	Lys	Phe	Ile	Arg	Glu	Cys	Ser	Val	Thr	Tyr	Leu	Phe	Lys	Asn	Met
			340					345					350		
Leu	Pro	Lys	Val	Ile	Asp	Glu	Leu	Asn	Glu	Phe	Asp	Arg	Asn	Thr	Lys
		355					360					365			
Ala	Lys	Leu	Ile	Asn	Leu	Ile	Asp	Ser	His	Asn	Ile	Ile	Leu	Val	Gly
	370					375					380				
Glu	Val	Asp	Lys	Leu	Lys	Ala	Lys	Val	Asn	Asn	Ser	Phe	Gln	Asn	
385					390					395					

<210> 25
 <211> 1161
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<221> CDS
 <222> (1)...(1158)

<400> 25
 atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac 48
 Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1 5 10 15

aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc 96
 Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
 20 25 30

gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac 144
 Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
 35 40 45

aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac 192
 Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
 50 55 60

cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg 240
 Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
 65 70 75 80

aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac 288
 Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
 85 90 95

gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct 336
 Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
 100 105 110

aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg 384
 Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
 115 120 125

ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag 432
 Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
 130 135 140

gtt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag 480
 Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
 145 150 155 160

gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac 528
 Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
 165 170 175

aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg	576
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu	
180 185 190	
aac atc ggt aac tcc gcc ctg aga ggt aac ttc aac cag gcc ttc gcc	624
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala	
195 200 205	
acc gcc ggt gtc gcc ttc ctg ctg gag ggt ttc cca gag ttc acc atc	672
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile	
210 215 220	
cca gcc ctg ggt gtc ttc acc ttc tac tcc tcc atc cag gag aga gag	720
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu	
225 230 235 240	
aag atc atc aag acc atc gag aac tgc ttg gag cag aga gtc aag aga	768
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg	
245 250 255	
tgg aag gac tcc tac cag tgg atg gtt tcc aac tgg ctg tcc aga atc	816
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile	
260 265 270	
acc acc caa ttc aac cac atc aac tac cag atg tac gac tcc ctg tcc	864
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser	
275 280 285	
tac cag gcc gac gcc atc aag gcc aag atc gac ctg gag tac aag aag	912
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys	
290 295 300	
tac tcc ggt tcc gac aag gag aac atc aag tcc cag gtc gag aac ctg	960
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu	
305 310 315 320	
aag aac tcc ttg gac gtc aag atc tcc gag gcc atg aac aac atc aac	1008
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn	
325 330 335	
aag ttc atc cgt gag tgt tcc gtc acc tac ctg ttc aag aac atg ctg	1056
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu	
340 345 350	
cca aag gtc atc gac gag ctg aac aag ttc gac ctg aga acc aag acc	1104
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr	
355 360 365	
gag ctg atc aac ctg atc gac tcc cac aac atc atc ctg gtt ggt gag	1152
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu	
370 375 380	
gtt gac taa	1161
Val Asp	
385	

<210> 26
<211> 386
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hn

<400> 26
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
1 5 10 15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
20 25 30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
35 40 45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
50 55 60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65 70 75 80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
85 90 95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
100 105 110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
115 120 125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
130 135 140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145 150 155 160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
165 170 175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
180 185 190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
195 200 205
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
210 215 220
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225 230 235 240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
245 250 255
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
260 265 270
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
275 280 285
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
290 295 300
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305 310 315 320
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
325 330 335
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
340 345 350
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
355 360 365
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu

370
Val Asp
385

375

380

<210> 27
<211> 1149
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (1)...(1146)

<400> 27

atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct 48
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
1 5 10 15

tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att 96
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
20 25 30

gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag 144
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
35 40 45

gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag 192
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
50 55 60

aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac 240
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65 70 75 80

tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac 288
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
85 90 95

gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac 336
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
100 105 110

gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag 384
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
115 120 125

atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct 432
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
130 135 140

gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac 480
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145 150 155 160

ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac 528
 Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
 165 170 175

atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac 576
 Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
 180 185 190

gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc 624
 Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
 195 200 205

ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg 672
 Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
 210 215 220

gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag 720
 Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
 225 230 235 240

gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg 768
 Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
 245 250 255

aag gaa gtc tat tcc ttc atc gtc tcg aac tgg atg acc aag atc aac 816
 Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
 260 265 270

acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac 864
 Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
 275 280 285

cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac 912
 Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
 290 295 300

acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag 960
 Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
 305 310 315 320

atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc 1008
 Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
 325 330 335

gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc 1056
 Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
 340 345 350

aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag 1104
 Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
 355 360 365

acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg 1146
 Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
 370 375 380

taa 1149

<210> 28
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTE Hn

<400> 28

Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
1 5 10 15
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
20 25 30
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
35 40 45
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
50 55 60
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65 70 75 80
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
85 90 95
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
100 105 110
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
115 120 125
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
130 135 140
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145 150 155 160
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
165 170 175
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
180 185 190
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
195 200 205
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
210 215 220
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225 230 235 240
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
245 250 255
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
260 265 270
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
275 280 285
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
290 295 300
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305 310 315 320
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
325 330 335
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
340 345 350
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
355 360 365

Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
 370 375 380

<210> 29
 <211> 1227
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BONTA Hc

<221> CDS
 <222> (1)...(1224)

<400> 29
 atg gcc cca cca cgt ctg tgt att aga gtc aac aac tca gaa tta ttc 48
 Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1 5 10 15
 ttt gtc gct tcc gag tca agc tac aac gag aac gat att aac aca cct 96
 Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
 20 25 30
 aaa gag att gac gat act acc aac cta aac aac aac tac cgg aac aac 144
 Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
 35 40 45
 ttg gat gag gtt att ttg gat tac aac tca cag acc atc cct caa att 192
 Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
 50 55 60
 tcc aac cgt acc tta aac act ctt gtc caa gac aac tcc tac gtt cca 240
 Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65 70 75 80
 aga tac gat tct aac ggt acc tca gag atc gag gag tat gat gtt gtt 288
 Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
 85 90 95
 gac ttt aac gtc ttt ttc tat ttg cat gcc cag aag gtg cca gaa ggt 336
 Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
 100 105 110
 gaa acc aac atc tca ttg act tct tcc att gat acc gcc ttg ttg gaa 384
 Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
 115 120 125
 gag tcc aag gat atc ttc ttt tct tcg gag ttt atc gat act atc aac 432
 Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
 130 135 140
 aag cct gtc aac gcc gct ctg ttc att gat tgg att agc aag gtc atc 480
 Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
 145 150 155 160
 aga gat ttt acc act gaa gct act caa aag tcc act gtt gat aag att 528

Arg	Asp	Phe	Thr	Thr	Glu	Ala	Thr	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile	
				165					170					175		
gct	gac	atc	tct	ttg	att	gtc	ccc	tat	gtc	ggg	ctt	gct	ttg	aac	atc	576
Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Val	Gly	Leu	Ala	Leu	Asn	Ile	
			180					185					190			
att	att	gag	gca	gaa	aag	ggg	aac	ttt	gag	gag	gct	ttt	gaa	ttg	ttg	624
Ile	Ile	Glu	Ala	Glu	Lys	Gly	Asn	Phe	Glu	Glu	Ala	Phe	Glu	Leu	Leu	
		195					200					205				
gga	gtt	ggg	att	ttg	ttg	gag	ttt	gtt	cca	gaa	ctt	acc	att	cct	gtc	672
Gly	Val	Gly	Ile	Leu	Leu	Glu	Phe	Val	Pro	Glu	Leu	Thr	Ile	Pro	Val	
	210					215					220					
att	tta	gtt	ttt	acg	atc	aag	tcc	tac	atc	gat	tca	tac	gag	aac	aag	720
Ile	Leu	Val	Phe	Thr	Ile	Lys	Ser	Tyr	Ile	Asp	Ser	Tyr	Glu	Asn	Lys	
225					230					235					240	
aat	aaa	gca	att	aaa	gct	att	aac	aac	tcc	ttg	atc	gaa	aga	gag	gct	768
Asn	Lys	Ala	Ile	Lys	Ala	Ile	Asn	Asn	Ser	Leu	Ile	Glu	Arg	Glu	Ala	
				245					250					255		
aag	tgg	aag	gaa	atc	tac	tca	tgg	att	gta	tca	aac	tgg	ctt	act	aga	816
Lys	Trp	Lys	Glu	Ile	Tyr	Ser	Trp	Ile	Val	Ser	Asn	Trp	Leu	Thr	Arg	
			260					265					270			
att	aac	act	caa	ttt	aac	aag	aga	aag	gag	caa	atg	tac	cag	gct	ctg	864
Ile	Asn	Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu	
		275					280					285				
caa	aac	caa	gtc	gat	gct	atc	aag	act	gca	att	gaa	tac	aag	tac	aac	912
Gln	Asn	Gln	Val	Asp	Ala	Ile	Lys	Thr	Ala	Ile	Glu	Tyr	Lys	Tyr	Asn	
	290					295					300					
aac	tat	act	tcc	gat	gag	aag	aac	aga	ctt	gaa	tct	gaa	tac	aat	atc	960
Asn	Tyr	Thr	Ser	Asp	Glu	Lys	Asn	Arg	Leu	Glu	Ser	Glu	Tyr	Asn	Ile	
305					310					315					320	
aac	aac	att	gaa	gaa	gag	ttg	aac	aag	aaa	gtt	tct	ttg	gct	atg	aag	1008
Asn	Asn	Ile	Glu	Glu	Glu	Leu	Asn	Lys	Lys	Val	Ser	Leu	Ala	Met	Lys	
				325					330					335		
aat	atc	gaa	aga	ttt	atg	acc	gaa	tcc	tct	atc	tct	tac	ttg	atg	aag	1056
Asn	Ile	Glu	Arg	Phe	Met	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys	
			340					345					350			
ttg	atc	aat	gag	gcc	aag	gtt	ggg	aag	ttg	aag	aag	tac	gat	aac	cac	1104
Leu	Ile	Asn	Glu	Ala	Lys	Val	Gly	Lys	Leu	Lys	Lys	Tyr	Asp	Asn	His	
		355					360					365				
gtt	aag	agc	gat	ctg	ctg	aac	tac	att	ctc	gac	cac	aga	tca	atc	ctg	1152
Val	Lys	Ser	Asp	Leu	Leu	Asn	Tyr	Ile	Leu	Asp	His	Arg	Ser	Ile	Leu	
	370					375					380					
gga	gag	cag	aca	aac	gag	ctg	agt	gat	ttg	gtt	act	tcc	act	ttg	aac	1200
Gly	Glu	Gln	Thr	Asn	Glu	Leu	Ser	Asp	Leu	Val	Thr	Ser	Thr	Leu	Asn	

385

390

395

400

tcc tcc att cca ttt gag ctt tct taa

1227

Ser Ser Ile Pro Phe Glu Leu Ser

405

<210> 30

<211> 408

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hn

<400> 30

Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe

1 5 10 15

Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro

20 25 30

Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn

35 40 45

Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile

50 55 60

Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro

65 70 75 80

Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val

85 90 95

Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly

100 105 110

Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu

115 120 125

Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn

130 135 140

Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile

145 150 155 160

Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile

165 170 175

Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile

180 185 190

Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu

195 200 205

Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val

210 215 220

Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys

225 230 235 240

Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala

245 250 255

Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg

260 265 270

Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu

275 280 285

Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn

290 295 300

Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile

305 310 315 320

a

Asn	Asn	Ile	Glu	Glu	Glu	Leu	Asn	Lys	Lys	Val	Ser	Leu	Ala	Met	Lys	
				325					330					335		
Asn	Ile	Glu	Arg	Phe	Met	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys	
			340					345					350			
Leu	Ile	Asn	Glu	Ala	Lys	Val	Gly	Lys	Leu	Lys	Lys	Tyr	Asp	Asn	His	
		355					360					365				
Val	Lys	Ser	Asp	Leu	Leu	Asn	Tyr	Ile	Leu	Asp	His	Arg	Ser	Ile	Leu	
	370					375					380					
Gly	Glu	Gln	Thr	Asn	Glu	Leu	Ser	Asp	Leu	Val	Thr	Ser	Thr	Leu	Asn	
385					390					395					400	
Ser	Ser	Ile	Pro	Phe	Glu	Leu	Ser									
				405												

<210> 31

<211> 1233

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BONTA Hc

<221> CDS

<222> (1)...(1230)

<400> 31

atg gcc aaa aat acc ggt aaa tct gaa cag tgt att att gtt aat aat 48

Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn

1

5

10

15

gag gat tta ttt ttc ata gct aat aaa gat agt ttt tca aaa gat tta 96

Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu

20

25

30

gct aaa gca gaa act ata gca tat aat aca caa aat aat act ata gaa 144

Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu

35

40

45

aat aat ttt tct ata gat cag ttg att tta gat aat gat tta agc agt 192

Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser

50

55

60

ggc ata gac tta cca aat gaa aac aca gaa cca ttt aca aat ttt gac 240

Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp

65

70

75

80

gac ata gat atc cct gtg tat att aaa caa tct gct tta aaa aaa att 288

Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile

85

90

95

ttt gtg gat gga gat agc ctt ttt gaa tat tta cat gct caa aca ttt 336

Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe

100

105

110

cct tct aat ata gaa aat cta caa cta acg aat tca tta aat gat gct 384

Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala

115

120

125

tta aga aat aat aat aaa gtc tat act ttt ttt tct aca aac ctt gtt	432
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val	
130 135 140	
gaa aaa gct aat aca gtt gta ggt gct tca ctt ttt gta aac tgg gta	480
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val	
145 150 155 160	
aaa gga gta ata gat gat ttt aca tct gaa tcc aca caa aaa agt act	528
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr	
165 170 175	
ata gat aaa gtt tca gat gta tcc ata att att ccc tat ata gga cct	576
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro	
180 185 190	
gct ttg aat gta gga aat gaa aca gct aaa gaa aat ttt aaa aat gct	624
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala	
195 200 205	
ttt gaa ata ggt gga gcc gct atc tta atg gag ttt att cca gaa ctt	672
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu	
210 215 220	
att gta cct ata gtt gga ttt ttt aca tta gaa tca tat gta gga aat	720
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn	
225 230 235 240	
aaa ggg cat att att atg acg ata tcc aat gct tta aag aaa agg gat	768
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp	
245 250 255	
caa aaa tgg aca gat atg tat ggt ttg ata gta tcg cag tgg ctc tca	816
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser	
260 265 270	
acg gtt aat act caa ttt tat aca ata aaa gaa aga atg tac aat gct	864
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala	
275 280 285	
tta aat aat caa tca caa gca ata gaa aaa ata ata gaa gat caa tat	912
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr	
290 295 300	
aat aga tat agt gaa gaa gat aaa atg aat att aac att gat ttt aat	960
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn	
305 310 315 320	
gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat	1008
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn	
325 330 335	
ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga	1056
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg	
340 345 350	

atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt	1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu	
355 360 365	
aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt	1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu	
370 375 380	
gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac	1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp	
385 390 395 400	
agt ata cca ttt gat ctt tca cta tat acc taa	1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr	
405 410	

<210> 32

<211> 410

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTG Hn

<400> 32

Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn	
1 5 10 15	
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu	
20 25 30	
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu	
35 40 45	
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser	
50 55 60	
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp	
65 70 75 80	
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile	
85 90 95	
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe	
100 105 110	
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala	
115 120 125	
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val	
130 135 140	
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val	
145 150 155 160	
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr	
165 170 175	
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Pro Tyr Ile Gly Pro	
180 185 190	
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala	
195 200 205	
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu	
210 215 220	
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn	
225 230 235 240	

Ile	Ile	Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val		
80						85					90						
cgt	atc	ccg	aaa	tac	ttc	aac	aaa	gtt	aac	ctg	aac	aac	gaa	tac	act	339	
Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	110	
95					100				105								
atc	atc	gac	tgc	atc	cgt	aac	aac	aac	tct	ggg	tgg	aaa	atc	tct	ctg	387	
Ile	Ile	Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	125	
				115					120								
aac	tac	aac	aaa	atc	atc	tgg	act	ctg	cag	gac	act	gct	ggg	aac	aac	435	
Asn	Tyr	Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	140	
			130					135									
cag	aaa	ctg	gtt	ttc	aac	tac	act	cag	atg	atc	tct	atc	tct	gac	tac	483	
Gln	Lys	Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	155	
			145					150									
att	aac	aaa	tgg	atc	ttc	gtt	act	atc	act	aac	aac	cgt	ctg	ggg	aac	531	
Ile	Asn	Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	170	
			160					165									
tct	cgt	atc	tac	atc	aac	ggg	aac	ctg	atc	gat	gaa	aaa	tct	atc	tct	579	
Ser	Arg	Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	190	
					180					185							
aac	ctg	ggg	gac	atc	cac	gtt	tct	gac	aac	atc	ctg	ttc	aaa	atc	gtt	627	
Asn	Leu	Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	205	
				195					200								
ggg	tgc	aac	gac	acg	cgt	tac	gtt	ggg	atc	cgt	tac	ttc	aaa	gtt	ttc	675	
Gly	Cys	Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	220	
				210				215									
gac	act	gaa	ctg	ggg	aaa	act	gaa	atc	gaa	act	ctg	tac	tct	gac	gaa	723	
Asp	Thr	Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	235	
				225				230									
ccg	gac	ccg	tct	atc	ctg	aaa	gac	ttc	tgg	ggg	aac	tac	ctg	ctg	tac	771	
Pro	Asp	Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	250	
						245											
aac	aaa	cgt	tac	tac	ctg	ctg	aac	ctg	ctc	cgg	act	gac	aaa	tct	atc	819	
Asn	Lys	Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	270	
					260					265							
act	cag	aac	tct	aac	ttc	ctg	aac	atc	aac	cag	cag	cgt	ggg	gtt	tat	867	
Thr	Gln	Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	285	
				275					280								
cag	aaa	cct	aac	atc	ttc	tct	aac	act	cgt	ctg	tac	act	ggg	gtt	gaa	915	
Gln	Lys	Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	300	
				290				295									
gtt	atc	atc	cgt	aaa	aac	ggg	tct	act	gac	atc	tct	aac	act	gac	aac	963	
Val	Ile	Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn		

305 310 315
 ttc gta cgt aaa aac gac ctg gct tac atc aac gtt gtt gac cgt gac 1011
 Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
 320 325 330
 gtt gaa tac cgt ctg tac gct gac atc tct atc gct aaa ccg gaa aaa 1059
 Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
 335 340 345 350
 atc atc aaa ctg atc cgt act tct aac tct aac aac tct ctg ggt cag 1107
 Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
 355 360 365
 atc atc gtt atg gac tcg atc ggt aac aac tgc act atg aac ttc cag 1155
 Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
 370 375 380
 aac aac aac ggt ggt aac atc ggt ctg ctg ggt ttc cac tct aac aac 1203
 Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
 385 390 395
 ctg gtt gct tct tca tgg tac tac aac aac atc cgt aaa aac act tct 1251
 Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
 400 405 410
 tct aac ggt tgc ttc tgg tct ttc atc tct aaa gaa cac ggt tgg cag 1299
 Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
 415 420 425 430
 gaa aac taagaattc 1314
 Glu Asn

<210> 34
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTF Hc

<400> 34
 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
 1 5 10 15
 Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
 20 25 30
 Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
 35 40 45
 Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
 50 55 60
 Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
 65 70 75 80
 Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
 85 90 95

Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
 100 105 110
 Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
 115 120 125
 Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
 130 135 140
 Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
 145 150 155 160
 Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
 165 170 175
 Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
 180 185 190
 Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
 195 200 205
 Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
 210 215 220
 Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
 225 230 235 240
 Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
 245 250 255
 Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
 260 265 270
 Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
 275 280 285
 Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
 290 295 300
 Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
 305 310 315 320
 Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
 325 330 335
 Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
 340 345 350
 Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
 355 360 365
 Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
 370 375 380
 Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
 385 390 395 400
 Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
 405 410 415
 Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
 420 425 430

<210> 35

<211> 1278

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BONTA Hc

<221> CDS

<222> (10)...(1269)

<400> 35

ttcgaacg atg att tta att tcc tac ttc aac aag ttc ttc aag aga att 51

Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile
 1 5 10

aag tct tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc 99
 Lys Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val
 15 20 25 30

gac act tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac 147
 Asp Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr
 35 40 45

aag tac cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt 195
 Lys Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu
 50 55 60

act gag ctg aac atc tct caa aac gac tac att atc tac gac aac aag 243
 Thr Glu Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys
 65 70 75

tac aat aac ttc tct att tct ttc tgg gtc aga att cct aac tac gat 291
 Tyr Asn Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp
 80 85 90

aac aag atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg 339
 Asn Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
 95 100 105 110

aga gac aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atg 387
 Arg Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Met
 115 120 125

att tgg acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc 435
 Ile Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe
 130 135 140

aac tac ggt aac gca aac ggt att tct gac tac atc aac aag tgg att 483
 Asn Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile
 145 150 155

ttc gtc act atc act aac gac aga tta ggg gac tct aag ctt tac att 531
 Phe Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile
 160 165 170

aac ggt aac tta atc gac caa aag tcc att tta aac tta ggt aac att 579
 Asn Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile
 175 180 185 190

cac gtt tct gac aac atc tta ttc aag atc gtt aac tgc agt tac aac 627
 His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Asn
 195 200 205

aga tac att ggc att aga tac ttc aac att ttc gac aag gag tta gac 675
 Arg Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp
 210 215 220

gag acc gag att caa act tta tac agc aac gaa cct aac acc aat att 723
 Glu Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile

225	230	235	
ttg aag gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac			771
Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr			
240	245	250	
tta tta aac gtg tta aag cca aac aac ttc att gat agg aga aag gat			819
Leu Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp			
255	260	265	270
tct act tta agc att aac aac atc aga agc act att ctt tta gct aac			867
Ser Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn			
275	280	285	
aga tta tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct			915
Arg Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser			
290	295	300	
tct act aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac			963
Ser Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn			
305	310	315	
ttc gtc gct agc aag act cac tta ttc cca tta tat gct gat aac gct			1011
Phe Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Asn Ala			
320	325	330	
acc acc aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga			1059
Thr Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg			
335	340	345	350
ttt aac caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg			1107
Phe Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met			
355	360	365	
aac ttt aaa aat aat aat gga aat aat att ggg tgt tta ggt ttc aag			1155
Asn Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Cys Leu Gly Phe Lys			
370	375	380	
gca gat act gta gtt gct agt act tgg tat tat acc cac atg aga gat			1203
Ala Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp			
385	390	395	
cac acc aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat			1251
His Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His			
400	405	410	
gga tgg caa gaa aaa taa tagggatcc			1278
Gly Trp Gln Glu Lys *			
415			

<210> 36

<211> 419

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BONTE Hc

<400> 36

Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
1 5 10 15
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
20 25 30
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
35 40 45
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu
50 55 60
Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
65 70 75 80
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
85 90 95
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
100 105 110
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
115 120 125
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr
130 135 140
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val
145 150 155 160
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly
165 170 175
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val
180 185 190
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr
195 200 205
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr
210 215 220
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys
225 230 235 240
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu
245 250 255
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr
260 265 270
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu
275 280 285
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr
290 295 300
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val
305 310 315 320
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr
325 330 335
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn
340 345 350
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe
355 360 365
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp
370 375 380
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr
385 390 395 400
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
405 410 415
Gln Glu Lys

<210> 37
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (9)...(1325)

<400> 37

ctcgagcc atg gct cgt ctg ctg tct acc ttc act gaa tac atc aag aac 50
Met Ala Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
1 5 10

atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg 98
Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
15 20 25 30

atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt 146
Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
35 40 45

aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa 194
Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
50 55 60

tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct 242
Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
65 70 75

atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac 290
Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
80 85 90

ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg 338
Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
95 100 105 110

gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc 386
Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
115 120 125

tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa 434
Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
130 135 140

tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc 482
Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
145 150 155

gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac 530
Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn

160	165	170	
ggc cgt ctg atc gac cag	aaa ccg atc tcc aat ctg ggt aac atc cac	578	
Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His			
175	180 185 190		
gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac	626		
Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His			
195 200 205			
cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac	674		
Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn			
210 215 220			
gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc	722		
Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile			
225 230 235			
ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac	770		
Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr			
240 245 250			
atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta	818		
Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val			
255 260 265 270			
ggg atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg	866		
Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met			
275 280 285			
act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc	914		
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe			
290 295 300			
atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac	962		
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn			
305 310 315			
aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt	1010		
Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg			
320 325 330			
ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct	1058		
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala			
335 340 345 350			
ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa	1106		
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys			
355 360 365			
tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag	1154		
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln			
370 375 380			
gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac	1202		
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn			
385 390 395			

aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa 1250
 Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
 400 405 410

cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat 1298
 Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
 415 420 425 430

gac ggt tgg ggt gaa cgt ccg ctg taa cccgggaaag ctt 1338
 Asp Gly Trp Gly Glu Arg Pro Leu *
 435

<210> 38
 <211> 415
 <212> PRT
 <213> Clostridium botulinum

<400> 38
 Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
 1 5 10 15
 Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln
 20 25 30
 Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys
 35 40 45
 Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
 50 55 60
 Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
 65 70 75 80
 Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
 85 90 95
 Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile
 100 105 110
 Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
 115 120 125
 Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
 130 135 140
 Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile
 145 150 155 160
 Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu
 165 170 175
 Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Phe Tyr Phe Asn
 180 185 190
 Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp
 195 200 205
 Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu
 210 215 220
 Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys
 225 230 235 240
 Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys
 245 250 255
 Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser
 260 265 270
 Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn
 275 280 285
 Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val

290		295		300
Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly				
305		310		315
Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu				
	325		330	335
Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn				
	340		345	350
Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe				
	355		360	365
Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn				
	370		375	380
Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser				
385		390		395
Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu				
	405		410	415

<210> 39
 <211> 1348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hc

<221> CDS
 <222> (1)...(1323)

Q

<400> 39	
atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc ctg aac	48
Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn	
1 5 10 15	
ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac ggt gct	96
Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala	
20 25 30	
aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac cag ttc	144
Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe	
35 40 45	
aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag aat cag	192
Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln	
50 55 60	
aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc ttc tgg	240
Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp	
65 70 75 80	
atc cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac atc cac	288
Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His	
85 90 95	
aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt tgg aag	336
Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys	
100 105 110	

atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat atc aac	384
Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn	
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ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa gac atc	432
Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile	
130 135 140	
tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat aac ctg	480
Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu	
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Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp	
165 170 175	
atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc ttc aaa	576
Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys	
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ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa tac ttc	624
Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe	
195 200 205	
tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa cgg tac	672
Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr	
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Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro	
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ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac aag aac	768
Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn	
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tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc ctg act	816
Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr	
260 265 270	
cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc gac ctg	864
Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu	
275 280 285	
tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct cag tcc	912
Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser	
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Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe	
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Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys	
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 Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr
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 Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile
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 Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu
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 Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val
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 Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile
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 35 40 45
 Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln Asn
 50 55 60
 Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp Ile
 65 70 75 80
 Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His Asn
 85 90 95
 Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys Ile
 100 105 110
 Ser Ile Arg Gly Asn Arg Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys
 115 120 125
 Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu
 130 135 140
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 145 150 155 160
 Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys
 165 170 175

Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu Asp
 180 185 190
 Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile
 195 200 205
 Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys Ile
 210 215 220
 Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu Met
 225 230 235 240
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 245 250 255
 Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg Ser
 260 265 270
 Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr Ile
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 Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn
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 Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn
 305 310 315 320
 Leu Asn Gln Glu Arg Val Tyr Thr Tyr Lys Phe Lys Lys Glu Glu Glu
 325 330 335
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 Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln Leu
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 Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly
 370 375 380
 Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys Asp
 385 390 395 400
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 Gly Trp Thr Glu
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 Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
 65 70 75 80
 Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
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 Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
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 Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
 165 170 175
 Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
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 Leu Asn Ile Gly Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile
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 Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val
 225 230 235 240
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 Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val
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 Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu
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 Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln
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 Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu
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 Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn
 325 330 335
 Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile
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 Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp
 355 360 365
 Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile Gly Gln
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 Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile
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 405 410 415
 Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu
 420 425 430
 Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
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 450 455 460
 Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys
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 Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
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 Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
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 Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
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 Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile
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 Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
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 Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
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 Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
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 Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Ile Leu Leu Tyr Asp Pro Asn
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 Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
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 Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
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 Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
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 Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
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 Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro Ser
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 Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val Tyr
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 Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr Ile
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 Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys Val

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 Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp Phe
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 Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn Glu
 180 185 190
 Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala Ser
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 Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys Thr
 225 230 235 240
 Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met Tyr
 245 250 255
 Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr
 260 265 270
 Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln Ala
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 Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys Glu
 290 295 300
 Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu Asn
 305 310 315 320
 Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn Gly
 325 330 335
 Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val Glu
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 Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu Lys
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 385 390 395 400
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 405 410 415
 Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn Leu Arg Tyr Lys Asp Asn
 420 425 430
 Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys Val Glu Val Tyr Asp
 435 440 445
 Gly Val Glu Leu Asn Asp Lys Asn Gln Phe Lys Leu Thr Ser Ser Ala
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 465 470 475 480
 Phe Leu Asp Phe Ser Val Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys
 485 490 495
 Asn Asp Gly Ile Gln Asn Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn
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 Cys Met Lys Asn Asn Ser Gly Trp Lys Ile Ser Ile Arg Gly Arg Ile
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 Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe
 530 535 540
 Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe
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 Phe Val Thr Ile Thr Asn Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn
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Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile
 580 585 590
 Ala Asn Gly Glu Ile Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr
 595 600 605
 Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser
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 Gln Ser Asn Ile Glu Glu Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr
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 Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile
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 Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp
 770 775 780
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 785 790 795 800
 Glu Ser Gly Ile Val Phe Glu Glu Lys Asp Phe Cys Ile Ser Trp Tyr
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 Leu Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp
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JUL 27 2001
TECH CENTER 1600/2900

<112> U.S. Army Medical Research & Material Command

<120> RECOMBINANT VACCINE AGAINST BOTULINUM
NEUROTOXIN

<130> A33626 067252.0105

<140> PCT/US00/12890

<141> 2000-05-12

<150> 60/133,865

<151> 1999-05-12

<150> 60/133,866

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Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
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ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg 339
Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
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Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
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tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa 435
Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
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Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
145 150 155
gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac 531
Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
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Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn
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Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met
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 Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
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 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp

Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
 Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
 Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
 Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
 Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
 Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
 Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
 Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
 Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
 Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
 Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
 Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
 Gly Glu Arg Pro Leu

<210> 3
 <211> 1323
 <212> DNA
 <213> Synthetic Construct

<220>

<221> CDS
 <222> (13)...(1314)
 <223> Synthetic Construct

<400> 3
 gaattcgaaa cg atg tct acc ttc act gaa tac atc aag aac atc atc aat 51
 Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
 1 5 10

 acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg 99
 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
 15 20 25

 tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat 147
 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
 30 35 40 45

 ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa 195
 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
 50 55 60

 atc gaa gtt atc ctg aag aat gct atc gta taa aac tct atg tac gaa 243
 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
 65 70 75

 aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc 291
 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
 80 85 90

 atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat 339
 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
 95 100 105

 tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg 387
 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
 110 115 120 125

 cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag 435

B4

Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
 130 135 140
 atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc 483
 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
 145 150 155
 acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg 531
 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
 160 165 170
 atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat 579
 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
 175 180 185
 aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc 627
 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
 190 195 200 205
 tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa 675
 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
 210 215 220
 atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac 723
 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
 225 230 235
 ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat 771
 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
 240 245 250
 ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc cgc 819
 Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
 255 260 265
 ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc aac 867
 Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
 270 275 280 285
 atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc aag 915
 Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
 290 295 300
 aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat cgt 963
 Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
 305 310 315
 gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct acc 1011
 Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
 320 325 330
 aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa atc 1059
 Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
 335 340 345
 ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag aac 1107
 Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
 350 355 360 365
 gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac aat 1155
 Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn

B4

370										375					380					
ggt	aac	gat	atc	ggt	ttc	atc	ggt	ttc	cac	cag	ttc	aac	aat	atc	gct	1203				
Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala					
385				390				395												
aaa	ctg	ggt	gct	tcc	aac	tgg	tac	aat	cgt	cag	atc	gaa	cgt	tcc	tct	1251				
Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser					
400				405				410												
cgc	act	ctg	ggt	tgc	tct	tgg	gag	ttc	atc	ccg	gtt	gat	gac	ggt	tgg	1299				
Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp					
415				420				425												
ggt	gaa	cgt	ccg	ctg	taagaatttc										1323					
Gly	Glu	Arg	Pro	Leu																
430																				

<210> 4
 <211> 434
 <212> PRT
 <213> Synthetic Construct

 <220>

B4

<400> 4

Met	Ser	Thr	Phe	Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser	Ile
1				5					10					15	
Leu	Asn	Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg	Tyr
			20					25					30		
Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp
		35					40					45			
Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val
	50					55					60				
Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser
65					70					75				80	
Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu
				85					90					95	
Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp
			100					105					110		
Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr
		115					120					125			
Gln	Glu	Ile	Lys	Gln	Arg	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile	Asn	
	130					135				140					
Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn
145					150					155				160	
Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp	Gln
			165						170					175	
Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile	Met
			180				185					190			
Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile	Lys
	195						200					205			
Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys	Asp
	210					215					220				
Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp	Gly
225					230					235				240	
Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr	Asp
			245						250					255	
Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr	Met

Tyr Leu Lys 260 Gly Pro Arg Gly Ser 265 Val Met Thr Thr Asn 270 Ile Tyr Leu
 275 280 285
 Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
 290 295 300
 Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile
 305 310 315 320
 Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser
 325 330 335
 Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val
 340 345 350
 Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly
 355 360 365
 Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp
 370 375 380
 Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val
 385 390 395 400
 Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
 405 410 415
 Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg
 420 425 430
 Pro Leu

<210> 5
 <211> 1326
 <212> DNA
 <213> Synthetic Construct

<220>
 <221> CDS
 <222> (13)...(1317)

<400> 5
 gaattcgaaa cg atg gcc tct acc ttc act gaa tac atc aag aac atc atc 51
 Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile
 1 5 10
 aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac 99
 Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp
 15 20 25
 ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc 147
 Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe
 30 35 40 45
 gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc 195
 Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser
 50 55 60
 aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac 243
 Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr
 65 70 75
 gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac 291
 Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn
 80 85 90

tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac 339
 Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn
 95 100 105

 aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act 387
 Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr
 110 115 120 125

 ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct 435
 Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser
 130 135 140

 cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc 483
 Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr
 145 150 155

 atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt 531
 Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg
 160 165 170

 ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct 579
 Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser
 175 180 185

 aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac 627
 Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr
 190 195 200 205

 atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa 675
 Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys
 210 215 220

 gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa 723
 Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
 225 230 235

 gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg 771
 Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu
 240 245 250

 aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc 819
 Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile
 255 260 265

 cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc 867
 Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr
 270 275 280 285

 aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc 915
 Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile
 290 295 300

 aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat 963
 Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp
 305 310 315

 cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct 1011
 Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala
 320 325 330

 acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa 1059

B4

Thr	Asn	Ala	Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu		
335						340					345						
atc	ccg	gac	gtt	ggg	aat	ctg	tct	cag	gta	gtt	gta	atg	aaa	tcc	aag	1107	
Ile	Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys		
350					355					360					365		
aac	gac	cag	ggg	atc	act	aac	aaa	tgc	aaa	atg	aat	ctg	cag	gac	aac	1155	
Asn	Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn		
				370					375					380			
aat	ggg	aac	gat	atc	ggg	ttc	atc	ggg	ttc	cac	cag	ttc	aac	aat	atc	1203	
Asn	Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile		
			385					390					395				
gct	aaa	ctg	gtt	gct	tcc	aac	tgg	tac	aat	cgt	cag	atc	gaa	cgt	tcc	1251	
Ala	Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser		
		400					405					410					
tct	cgc	act	ctg	ggg	tgc	tct	tgg	gag	ttc	atc	ccg	gtt	gat	gac	ggg	1299	
Ser	Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly		
	415					420					425						
tgg	ggg	gaa	cgt	ccg	ctg	taagaattc										1326	
Trp	Gly	Glu	Arg	Pro	Leu												
430					435												

<210> 6
 <211> 435
 <212> PRT
 <213> Synthetic Construct

<220>

<400> 6

Met	Ala	Ser	Thr	Phe	Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser		
1				5					10					15			
Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg		
		20						25					30				
Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile		
	35						40					45					
Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu		
	50					55					60						
Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe		
65				70					75					80			
Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser		
			85						90					95			
Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly		
		100						105					110				
Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp		
	115						120					125					
Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile		
	130					135					140						
Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn		
145				150						155				160			
Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp		
			165					170					175				
Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile		
		180						185					190				

B4

Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile
 195 200 205
 Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys
 210 215 220
 Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp
 225 230 235 240
 Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr
 245 250 255
 Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr
 260 265 270
 Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
 275 280 285
 Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr
 290 295 300
 Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr
 305 310 315 320
 Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala
 325 330 335
 Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp
 340 345 350
 Val Gly Asn Leu Ser Gln Val Val Met Lys Ser Lys Asn Asp Gln
 355 360 365
 Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn
 370 375 380
 Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu
 385 390 395 400
 Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr
 405 410 415
 Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
 420 425 430
 Arg Pro Leu
 435

<210> 7
 <211> 1341
 <212> DNA
 <213> Synthetic Construct

<220>

<221> CDS
 <222> (10)...(1329)

<400> 7
 gaattcacg atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc 51
 Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile
 1 5 10

ctg aac ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac 99
 Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr
 15 20 25 30

ggt gct aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac 147
 Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn
 35 40 45

cag ttc aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag 195
 Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln
 50 55 60

B4

aat cag aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc 243
 Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser
 65 70 75

ttc tgg att cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac 291
 Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr
 80 85 90

atc cac aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt 339
 Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly
 95 100 105 110

tgg aag atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat 387
 Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp
 115 120 125

atc aac ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa 435
 Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu
 130 135 140

gac atc tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat 483
 Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn
 145 150 155

aac ctg aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat 531
 Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn
 160 165 170

acc gac atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc 579
 Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile
 175 180 185 190

ttc aaa ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa 627
 Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys
 195 200 205

tac ttc tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa 675
 Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu
 210 215 220

cgg tac aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt 723
 Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly
 225 230 235

aat ccg ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac 771
 Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn
 240 245 250

aag aac tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc 819
 Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile
 255 260 265 270

ctg act cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc 867
 Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg
 275 280 285

gac ctg tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct 915
 Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser
 290 295 300

B4

cag tcc atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg 963
 Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu
 305 310 315
 gac ttc ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac 1011
 Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr
 320 325 330
 ttc aag aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc 1059
 Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser
 335 340 345 350
 gac gaa ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg 1107
 Asp Glu Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro
 355 360 365
 acc tac tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac 1155
 Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp
 370 375 380
 gaa atc ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta 1203
 Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val
 385 390 395
 ttc gaa gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag 1251
 Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys
 400 405 410
 gaa gtt aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag 1299
 Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln
 415 420 425 430
 ttc atc ccg aaa gac gaa ggt tgg acc gaa tagtaagaat tc 1341
 Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
 435 440

<210> 8
 <211> 440
 <212> PRT
 <213> Synthetic Construct

<220>

<400> 8
 Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1 5 10 15
 Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
 20 25 30
 Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
 35 40 45
 Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
 50 55 60
 Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
 65 70 75 80
 Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
 85 90 95
 Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
 100 105 110
 Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn

115 120 125
 Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
 130 135 140
 Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
 145 150 155 160
 Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
 165 170 175
 Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
 180 185 190
 Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
 195 200 205
 Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
 210 215 220
 Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
 225 230 235 240
 Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn
 245 250 255
 Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr
 260 265 270
 Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu
 275 280 285
 Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser
 290 295 300
 Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe
 305 310 315 320
 Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys
 325 330 335
 Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
 340 345 350
 Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr
 355 360 365
 Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile
 370 375 380
 Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu
 385 390 395 400
 Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val
 405 410 415
 Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile
 420 425 430
 Pro Lys Asp Glu Gly Trp Thr Glu
 435 440

<210> 9
 <211> 1371
 <212> DNA
 <213> Synthetic Construct

<220>

<221> CDS
 <222> (10)...(1359)

<400> 9
 gaattcacg atg acc atc cca ttc aac atc ttc tcc tac acc aac aac tcc 51
 Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser
 1 5 10

ctg ttg aag gac atc atc aac gag tac ttc aac aac atc aac gac tcc 99
 Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser

15	20	25	30	
aag atc ctg tcc ctg cag aac cgt aag aac acc ttg gtc gac acc tcc				147
Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser	35	40	45	
ggt tac aac gcc gag gtc tcc gag gag ggt gac gtc cag ctg aac cca				195
Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro	50	55	60	
atc ttc cca ttc gac ttc aag ctg ggt tcc tcc ggt gag gac aga ggt				243
Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly	65	70	75	
aag gtc atc gtc acc cag aac gag aac atc gtc tac aac tcc atg tac				291
Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr	80	85	90	
gag tcc ttc tcc atc tcc ttc tgg atc aga atc aac aag tgg gtc tcc				339
Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser	95	100	105	110
aac ttg cca ggt tac acc atc atc gac tcc gtc aag aac aac tcc ggt				387
Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly	115	120	125	
tgg tcc atc ggt atc atc tcc aac ttc ctg gtc ttc acc ctg aag cag				435
Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln	130	135	140	
aac gag gac tcc gag cag tcc atc aac ttc tcc tac gac atc tcc aac				483
Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn	145	150	155	
aac gct cct ggt tac aac aag tgg ttc ttc gtc acc gtc acc aac aac				531
Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn	160	165	170	
atg atg ggt aac atg aag atc tac atc aac ggt aag ctg atc gac acc				579
Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr	175	180	185	190
atc aag gtc aag gag ttg acc ggt atc aac ttc tcc aag acc atc acc				627
Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr	195	200	205	
ttc gag atc aac aag atc cca gac acc ggt ctg atc acc tcc gac tcc				675
Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser	210	215	220	
gac aac atc aac atg tgg atc cgt gac ttc tac atc ttc gcc aag gag				723
Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu	225	230	235	
ttg gac ggt aag gac atc aac atc ctg ttc aac tcc ttg cag tac acc				771
Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr	240	245	250	
aac gtc gtc aag gac tac tgg ggt aac gac ctg aga tac aac aag gag				819
Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu	255	260	265	270

B4

tac tac atg gtc aac atc gac tac ttg aac aga tac atg tac gcc aac 867
 Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn
 275 280 285

 tcc aga cag atc gtc ttc aac acc aga cgt aac aac aac gac ttc aac 915
 Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn
 290 295 300

 gag ggt tac aag atc atc atc aag cgt atc aga ggt aac acc aac gac 963
 Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp
 305 310 315

 acc aga gtc aga ggt ggt gac atc ctg tac ttc gac atg act atc aac 1011
 Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn
 320 325 330

 aac aag gcc tac aac ctg ttc atg aag aac gag acc atg tac gcc gac 1059
 Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp
 335 340 345 350

 aac cac tcc acc gag gac atc tac gcc atc ggt ctg cgt gag cag acc 1107
 Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr
 355 360 365

 aag gac atc aac gac aac atc atc ttc cag atc cag cca atg aac aac 1155
 Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn
 370 375 380

 act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag 1203
 Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu
 385 390 395

 aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt 1251
 Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly
 400 405 410

 ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt 1299
 Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly
 415 420 425 430

 aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc 1347
 Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val
 435 440 445

 cca gtc tcc gag taataggaat tc 1371
 Pro Val Ser Glu
 450

<210> 10
 <211> 450
 <212> PRT
 <213> Synthetic Construct

<220>

<400> 10
 Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu
 1 5 10 15

B4

Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile
 20 25 30
 Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr
 35 40 45
 Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe
 50 55 60
 Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
 65 70 75 80
 Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser
 85 90 95
 Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu
 100 105 110
 Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser
 115 120 125
 Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu
 130 135 140
 Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala
 145 150 155 160
 Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met
 165 170 175
 Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys
 180 185 190
 Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu
 195 200 205
 Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn
 210 215 220
 Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp
 225 230 235 240
 Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val
 245 250 255
 Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
 260 265 270
 Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg
 275 280 285
 Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly
 290 295 300
 Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg
 305 310 315 320
 Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys
 325 330 335
 Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His
 340 345 350
 Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp
 355 360 365
 Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr
 370 375 380
 Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile
 385 390 395 400
 Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp
 405 410 415
 Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr
 420 425 430
 Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val
 435 440 445
 Ser Glu
 450

<210> 11
 <211> 1374
 <212> DNA

<213> Synthetic Construct

<220>

<221> CDS

<222> (10)...(1362)

<400> 11

gaattcacg atg cgt ttg aag gct aag gtc aac gag tcc ttc gag aac acc 51
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr
1 5 10

atg cca ttc aac atc ttc tcc tac acc aac aac tcc ttg ttg aag gac 99
Met Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp
15 20 25 30

atc atc aac gag tac ttc aac tcc atc aac gag tcc aag atc ttg tcc 147
Ile Ile Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser
35 40 45

ttg cag aac aag aag aac gcc ttg gtc gac acc tcc ggt tac aac gcc 195
Leu Gln Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala
50 55 60

gag gtc aga gtc ggt gac aac gtc cag ttg aac acc atc tac acc aac 243
Glu Val Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn
65 70 75

gac ttc aag ttg tcc tct tcc ggt gac aag atc atc gtc aac ttg aac 291
Asp Phe Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn
80 85 90

aac aac atc ttg tac tcc gcc atc tac gag aac tcc tct gtc tcc ttc 339
Asn Asn Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe
95 100 105 110

tgg atc aag atc tcc aag gac ttg acc aac tcc cac aac gag tac acc 387
Trp Ile Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr
115 120 125

atc atc aac tcc atc gag cag aac tcc ggt tgg aag ttg tgt atc cgt 435
Ile Ile Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg
130 135 140

aac ggt aac atc gag tgg atc ttg cag gac gtc aac cgt aag tac aag 483
Asn Gly Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys
145 150 155

tcc ttg atc ttc gac tac tcc gag tcc ttg tcc cac acc ggt tac acc 531
Ser Leu Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr
160 165 170

aac aag tgg ttc ttc gtc acc atc acc aac aac atc atg ggt tac atg 579
Asn Lys Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met
175 180 185 190

aag ttg tac atc aac ggt gag ttg aag cag tcc cag aag atc gag gac 627
Lys Leu Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp
195 200 205

ctg gac gag gtc aag ctg gac aag acc atc gtc ttc ggt atc gac gag 675
Leu Asp Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu

210	215	220	
aac atc gac gag aac cag atg ttg tgg att cgt gac ttc aac atc ttc Asn Ile Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe 225 230 235			723
tcc aag gag ctg tcc aac gag gac atc aac atc gtc tac gag ggt cag Ser Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln 240 245 250			771
atc ctg agg aac gtc atc aag gac tac tgg ggt aac cca ctg aag ttc Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe 255 260 265 270			819
gac acc gag tac tac atc atc aac gac aac tac atc gac cgt tac atc Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile 275 280 285			867
gcc cca gag tcc aac gtc ctg gtc ctg gtc cag tac cct gac ctg tcc Ala Pro Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser 290 295 300			915
aag ctg tac acc ggt aac cct atc acc atc aag tcc gtc tcc gac aag Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys 305 310 315			963
aac cct tac tcc cgt atc ctg aac ggt gac aac atc atc ctg cac atg Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met 320 325 330			1011
ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile 335 340 345 350			1059
tac gcc acc cag ggt ggt gag tgt tcc cag aac tgt gtc tac gcc ctg Tyr Ala Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu 355 360 365			1107
aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile 370 375 380			1155
aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser 385 390 395			1203
ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg 400 405 410			1251
ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu 415 420 425 430			1299
acc aag ctg ctg tcc acc tcc tcc ttc tgg aag ttc atc tcc cgt gac Thr Lys Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp 435 440 445			1347
cca ggt tgg gtc gag taataggaat tc Pro Gly Trp Val Glu 450			1374

B4

<210> 12
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12
Met Arg Deu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
1 5 10 15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
20 25 30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
35 40 45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
50 55 60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65 70 75 80
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
85 90 95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
100 105 110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
115 120 125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
130 135 140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145 150 155 160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
165 170 175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
180 185 190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
195 200 205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
210 215 220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys
225 230 235 240
Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu
245 250 255
Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr
260 265 270
Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro
275 280 285
Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser Lys Leu
290 295 300
Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro
305 310 315 320
Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr
325 330 335
Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala
340 345 350
Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu
355 360 365
Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn
370 375 380
Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg
385 390 395 400

B4

Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser
 405 410 415
 Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys
 420 425 430
 Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly
 435 440 445
 Trp Val Glu
 450

<210> 13
 <211> 1400
 <212> DNA
 <213> Synthetic Construct

<220>
 <221> CDS
 <222> (10)...(1356)

<400> 13
 gaattcacc atg gga gag agt cag caa gaa cta aat tct atg gta act gat 51
 Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp
 1 5 10

acc cta aat aat agt att cct ttt aag ctt tct tct tat aca gat gat 99
 Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp
 15 20 25 30

aaa att tta att tcc tac ttc aac aag ttc ttc aag aga att aag tct 147
 Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
 35 40 45

tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc gac act 195
 Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
 50 55 60

tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac aag tac 243
 Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
 65 70 75

cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt tcc gag 291
 Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu
 80 85 90

gtc aac atc tct caa aac gac tac att atc tac gac aac aag tac aag 339
 Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
 95 100 105 110

aac ttc tct att tct ttc tgg gtc agg att cct aac tac gac aac aag 387
 Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
 115 120 125

atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg aga gac 435
 Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
 130 135 140

aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atc att tgg 483
 Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
 145 150 155

acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc aac tac 531

B4

Thr	Leu	Gln	Asp	Asn	Ala	Gly	Ile	Asn	Gln	Lys	Leu	Ala	Phe	Asn	Tyr		
160						165					170						
ggt	aac	gca	aac	ggt	att	tct	gac	tac	atc	aac	aag	tgg	att	ttc	gtc	579	
Gly	Asn	Ala	Asn	Gly	Ile	Ser	Asp	Tyr	Ile	Asn	Lys	Trp	Ile	Phe	Val		
175					180					185					190		
act	atc	act	aac	gac	aga	tta	ggt	gac	tct	aag	ctt	tac	att	aac	ggt	627	
Thr	Ile	Thr	Asn	Asp	Arg	Leu	Gly	Asp	Ser	Lys	Leu	Tyr	Ile	Asn	Gly		
			195					200						205			
aac	tta	atc	gac	caa	aag	tcc	att	tta	aac	tta	ggt	aac	att	cac	gtt	675	
Asn	Leu	Ile	Asp	Gln	Lys	Ser	Ile	Leu	Asn	Leu	Gly	Asn	Ile	His	Val		
			210					215					220				
tct	gac	aac	atc	tta	ttc	aag	atc	gtt	aac	tgc	agt	tac	acc	aga	tac	723	
Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Asn	Cys	Ser	Tyr	Thr	Arg	Tyr		
		225					230					235					
att	ggc	att	aga	tac	ttc	aac	att	ttc	gac	aag	gag	tta	gac	gag	acc	771	
Ile	Gly	Ile	Arg	Tyr	Phe	Asn	Ile	Phe	Asp	Lys	Glu	Leu	Asp	Glu	Thr		
	240					245					250						
gag	att	caa	act	tta	tac	agc	aac	gaa	cct	aac	acc	aat	att	ttg	aag	819	
Glu	Ile	Gln	Thr	Leu	Tyr	Ser	Asn	Glu	Pro	Asn	Thr	Asn	Ile	Leu	Lys		
	255				260					265					270		
gac	ttc	tgg	ggt	aac	tac	ttg	ctt	tac	gac	aag	gaa	tac	tac	tta	tta	867	
Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asp	Lys	Glu	Tyr	Tyr	Leu	Leu		
			275					280						285			
aac	gtg	tta	aag	cca	aac	aac	ttc	att	gat	agg	aga	aag	gat	tct	act	915	
Asn	Val	Leu	Lys	Pro	Asn	Asn	Phe	Ile	Asp	Arg	Arg	Lys	Asp	Ser	Thr		
		290						295					300				
tta	agc	att	aac	aac	atc	aga	agc	act	att	ctt	tta	gct	aac	aga	tta	963	
Leu	Ser	Ile	Asn	Asn	Ile	Arg	Ser	Thr	Ile	Leu	Leu	Ala	Asn	Arg	Leu		
		305						310				315					
tac	tct	ggt	atc	aag	gtt	aag	atc	caa	aga	gtt	aac	aac	tct	tct	act	1011	
Tyr	Ser	Gly	Ile	Lys	Val	Lys	Ile	Gln	Arg	Val	Asn	Asn	Ser	Ser	Thr		
		320				325					330						
aac	gat	aac	ctt	gtt	aga	aag	aac	gat	cag	gtc	tat	att	aac	ttc	gtc	1059	
Asn	Asp	Asn	Leu	Val	Arg	Lys	Asn	Asp	Gln	Val	Tyr	Ile	Asn	Phe	Val		
	335				340					345					350		
gct	agc	aag	act	cac	tta	ttc	cca	tta	tat	gct	gat	acc	gct	acc	acc	1107	
Ala	Ser	Lys	Thr	His	Leu	Phe	Pro	Leu	Tyr	Ala	Asp	Thr	Ala	Thr	Thr		
			355					360					365				
aac	aag	gag	aag	acc	atc	aag	atc	tcc	tcc	tct	ggc	aac	aga	ttt	aac	1155	
Asn	Lys	Glu	Lys	Thr	Ile	Lys	Ile	Ser	Ser	Ser	Gly	Asn	Arg	Phe	Asn		
		370						375					380				
caa	gtc	gtc	gtt	atg	aac	tcc	gtc	ggt	aac	aac	tgt	acc	atg	aac	ttt	1203	
Gln	Val	Val	Val	Met	Asn	Ser	Val	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe		
		385					390					395					
aaa	aat	aat	aat	gga	aat	aat	att	ggg	ttg	tta	ggt	ttc	aag	gca	gat	1251	
Lys	Asn	Asn	Asn	Gly	Asn	Asn	Ile	Gly	Leu	Leu	Gly	Phe	Lys	Ala	Asp		

B4

400

405

410

act gta gtt gct agt act tgg tat tat acc cac atg aga gat cac acc 1299
 Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr
 415 420 425 430

aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat gga tgg 1347
 Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
 435 440 445

caa gaa aaa taatagggat ccgcggccgc acgcgtcccg ggactagtga 1396
 Gln Glu Lys

attc 1400

<210> 14

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 14

Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu
 1 5 10 15
 Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile
 20 25 30
 Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser
 35 40 45
 Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly
 50 55 60
 Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr
 65 70 75 80
 Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu Val Asn
 85 90 95
 Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe
 100 105 110
 Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val
 115 120 125
 Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn
 130 135 140
 Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
 145 150 155 160
 Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
 165 170 175
 Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
 180 185 190
 Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
 195 200 205
 Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
 210 215 220
 Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
 225 230 235 240
 Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
 245 250 255
 Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
 260 265 270
 Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
 275 280 285

04

Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
 290 295 300
 Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser
 305 310 315 320
 Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp
 325 330 335
 Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser
 340 345 350
 Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys
 355 360 365
 Glu Lys Thr Ile Lys Ile Ser Ser Gly Asn Arg Phe Asn Gln Val
 370 375 380
 Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn
 385 390 395 400
 Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val
 405 410 415
 Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn Ser
 420 425 430
 Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu
 435 440 445
 Lys

<210> 15
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (10)...(1305)

<400> 15
 gaattcagc atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51
 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
 1 5 10
 aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac 99
 Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15 20 25 30
 gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc 147
 Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
 35 40 45
 atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga 195
 Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
 50 55 60
 atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac 243
 Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
 65 70 75
 atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc 291
 Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
 80 85 90
 cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc 339

B4

Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
 95 100 105 110
 atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg 387
 Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
 115 120 125
 aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat 435
 Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
 130 135 140
 cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac 483
 Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
 145 150 155
 atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac 531
 Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
 160 165 170
 tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc 579
 Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
 175 180 185
 aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc 627
 Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
 195 200 205
 ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc 675
 Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe
 210 215 220
 gac act gag ttg ggt aag acc gag atc gag acc ttg tac tcc gac gag 723
 Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu
 225 230 235
 cct gac cca tcc atc ctg aag gac ttc tgg ggt aac tac ctg ctg tac 771
 Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
 240 245 250
 aac aaa cgt tac tac ttg ctg aac ttg ttg cgt acc gac aag tcc atc 819
 Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
 255 260 265 270
 acc cag aac tcc aac ttc ttg aac atc aac cag cag aga ggt gtc tac 867
 Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
 275 280 285
 cag aag cca aac atc ttc tcc aac acc aga ttg tac acc gga gtc gag 915
 Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
 290 295 300
 gtc att atc aga aag aac gga tct act gat att tcc aac acc gat aac 963
 Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
 305 310 315
 ttc gtc aga aag aac gat ctg gct tac atc aac gtt gtc gac aga gat 1011
 Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
 320 325 330
 gtc gaa tac cgt ctg tac gcc gat atc tct atc gcc aaa cct gaa aag 1059
 Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys

Bf

335	340	345	350	
atc atc aag ctg atc cgt acc tct aac tct aac aac tct ctg gga caa	1107			
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln				
355 360 365				
atc atc gtc atg gac tcc atc ggt aat aac tgt acc atg aac ttc cag	1155			
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln				
370 375 380				
aac aac aac ggt gga aac atc ggt ttg ttg ggt ttc cac tcc aac aac	1203			
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn				
385 390 395				
ttg gtc gct tcc tcc tgg tac tac aac aac atc cgt aag aac acc tcc	1251			
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser				
400 405 410				
tcc aac ggt tgc ttc tgg tcc ttc atc tcc aag gag cac ggt tgg cag	1299			
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln				
415 420 425 430				
gag aac taataggaat tc	1317			
Glu Asn				

<210> 16
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16

Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu	
1 5 10 15	
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn	
20 25 30	
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn	
35 40 45	
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr	
50 55 60	
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile	
65 70 75 80	
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile	
85 90 95	
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile	
100 105 110	
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr	
115 120 125	
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys	
130 135 140	
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn	
145 150 155 160	
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg	
165 170 175	
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu	
180 185 190	
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys	

B4

195 200 205
 Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
 210 215 220
 Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
 225 230 235 240
 Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
 245 250 255
 Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
 260 265 270
 Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
 275 280 285
 Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
 290 295 300
 Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
 305 310 315 320
 Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
 325 330 335
 Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
 340 345 350
 Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
 355 360 365
 Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
 370 375 380
 Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
 385 390 395 400
 Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
 405 410 415
 Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
 420 425 430

<210> 17
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (10)...(1356)

<400> 17
 gaattcacg atg aag gac acc atc ctg atc cag gtc ttc aac aac tac atc 51
 Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile
 1 5 10

 tcc aac atc tcc tcc aac gcc atc ctg tcc ctg tcc tac cgt ggt ggt 99
 Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly
 15 20 25 30

 cgt ctg atc gac tcc tcc ggt tac gga gcc acc atg aac gtc ggt tcc 147
 Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser
 35 40 45

 gac gtc atc ttc aac gac atc ggt aac ggt cag ttc aag ctg aac aac 195
 Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn
 50 55 60

 tcc gag aac tcc aac atc acc gcc cac cag tcc aag ttc gtc gtc tac 243
 Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr

65	70	75	
gac tcc atg ttc gac aac ttc tcc atc aac ttc tgg gtc cgt acc cca Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro			291
80	85	90	
aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr			339
95	100	105	110
atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys			387
115	120		125
gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys			435
130	135		140
tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile			483
145	150		155
aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala			531
160	165		170
aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn			579
175	180		185
ctg gac cgt atc aac tcc tcc aac gac atc gac ttc aag ctg atc aac Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn			627
195	200		205
tgt acc gac acc acc aag ttc gtc tgg atc aag gac ttc aac atc ttc Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe			675
210	215		220
ggt cgt gag ctg aac gcc acc gag gtc tcc tcc ctg tac tgg atc cag Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln			723
225	230		235
tcc tcc acc aac acc ctg aag gac ttc tgg gga aac cca ctg cgt tac Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr			771
240	245		250
gac acc cag tac tac ctg ttc aac cag ggt atg cag aac atc tac atc Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile			819
255	260		265
aag tac ttc tcc aag gcc tcc atg ggt gag acc gcc cct cgt acc aac Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn			867
275	280		285
ttc aac aac gcc gcc atc aac tac cag aac ctg tac ctg ggt ctg cgt Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg			915
290	295		300
ttc atc atc aag aag gcc tcc aac tcc cgt aac atc aac aac gac aac Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn			963
305	310		315

B4

atc gtc cgt gag ggt gac tac atc tac ctg aac atc gac aac atc tcc 1011
 Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser
 320 325 330
 gac gag tcc tac cgt gtc tac gtc ctg gtc aac tcc aag gag atc cag 1059
 Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln
 335 340 345 350
 acc cag ctg ttc ctg gcc cca atc aac gac gac cct acc ttc tac gac 1107
 Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp
 355 360 365
 gtc ctg cag atc aag aag tac tac gag aag acc acc tac aac tgt cag 1155
 Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln
 370 375 380
 atc ctg tgc gag aag gac acc aag acc ttc gga ctg ttc ggt atc ggt 1203
 Ile Leu Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly
 385 390 395
 aag ttc gtc aag gac tac ggt tac gtc tgg gac acc tac gac aac tac 1251
 Lys Phe Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr
 400 405 410
 ttc tgt atc tcc cag tgg tac ctg cgt cgt atc tcc gag aac atc aac 1299
 Phe Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn
 415 420 425 430
 aag ctg cgt ctg gga tgt aac tgg cag ttc atc cca gtc gac gag ggt 1347
 Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly
 435 440 445
 tgg acc gag taataggaat tc 1368
 Trp Thr Glu

<210> 18
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18
 Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
 1 5 10 15
 Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
 20 25 30
 Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
 35 40 45
 Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
 50 55 60
 Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser
 65 70 75 80
 Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr
 85 90 95
 Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile
 100 105 110

Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn
 115 120 125
 Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile
 130 135 140
 Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys
 145 150 155 160
 Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile
 165 170 175
 Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp
 180 185 190
 Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr
 195 200 205
 Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg
 210 215 220
 Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser
 225 230 235 240
 Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
 245 250 255
 Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr
 260 265 270
 Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn
 275 280 285
 Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile
 290 295 300
 Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
 305 310 315 320
 Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
 325 330 335
 Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln
 340 345 350
 Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu
 355 360 365
 Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu
 370 375 380
 Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe
 385 390 395 400
 Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys
 405 410 415
 Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu
 420 425 430
 Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr
 435 440 445
 Glu

<210> 19
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1239)

<400> 19
 atg gct ctg aac gac ctg tgc atc aaa gtt aac aac tgg gac ctg ttc 48
 Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1 5 10 15

ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa 96
 Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
 20 25 30
 gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct 144
 Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
 35 40 45
 ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa 192
 Leu Asp Leu Ile Gln Gln Tyr Leu Thr Phe Asn Phe Asp Asn Glu
 50 55 60
 ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag 240
 Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
 65 70 75 80
 ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac 288
 Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
 85 90 95
 gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc 336
 Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
 100 105 110
 gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct 384
 Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
 115 120 125
 ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt 432
 Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
 130 135 140
 aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt 480
 Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
 145 150 155 160
 gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc 528
 Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
 165 170 175
 act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg 576
 Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
 180 185 190
 gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct 624
 Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
 195 200 205
 ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc 672
 Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
 210 215 220
 gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac 720
 Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
 225 230 235 240
 aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac 768
 Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
 245 250 255

B4

gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct 816
 Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
 260 265 270
 aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct 864
 Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
 275 280 285
 ctg gaa aac cag gct gaa gct act aaa gct atc atc aac tac cag tac 912
 Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
 290 295 300
 aac cag tac acc gaa gaa gaa aag aac aac atc aac ttc aac atc gat 960
 Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
 305 310 315 320
 gac ctg tcc tct aaa ctg aac gaa tcc atc aac aaa gct atg atc aac 1008
 Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
 325 330 335
 atc aac aaa ttc ctg aac cag tgc tct gtt tcc tac ctg atg aac tct 1056
 Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
 340 345 350
 atg atc ccg tac ggc gtt aaa cgc ctg gaa gac ttc gac gct tcc ctg 1104
 Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
 355 360 365
 aaa gac gct ctg ctg aaa tac atc cgt gac aac tac ggt act ctg atc 1152
 Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
 370 375 380
 ggc cag gtt gac cgt ctg aaa gac aag gtt aac aac acc ctg tct act 1200
 Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
 385 390 395 400
 gac atc ccg ttc cag ctg tcc aaa tac gtt gac aac cag taa 1242
 Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
 405 410

<210> 20
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20
 Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1 5 10 15
 Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
 20 25 30
 Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
 35 40 45
 Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
 50 55 60
 Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
 65 70 75 80
 Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr

85 90 95
 Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
 100 105 110
 Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
 115 120 125
 Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
 130 135 140
 Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
 145 150 155 160
 Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
 165 170 175
 Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Pro Tyr Ile Gly Pro
 180 185 190
 Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
 195 200 205
 Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
 210 215 220
 Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
 225 230 235 240
 Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
 245 250 255
 Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
 260 265 270
 Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
 275 280 285
 Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
 290 295 300
 Asn Gln Tyr Thr Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
 305 310 315 320
 Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
 325 330 335
 Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
 340 345 350
 Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
 355 360 365
 Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
 370 375 380
 Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
 385 390 395 400
 Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
 405 410

<210> 21
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1239)

<400> 21
 atg gct cca gga atc tgt atc gac gtc gac aac gag gac ttg ttc ttc 48
 Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
 1 5 10 15
 atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga 96
 Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg

20	25	30	
atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile	144		
35	40	45	
aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro	192		
50	55	60	
tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val	240		
65	70	75	80
tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr	288		
85	90	95	
atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp	336		
100	105	110	
atc tcc ttg acc tct tcc ttc gac gac gcc ctg ctg ttc tcc aac aag Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys	384		
115	120	125	
gtc tac tcc ttc ttc tcc atg gac tac atc aag act gct aac aag gtc Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val	432		
130	135	140	
gtc gag gcc ggt ttg ttc gct ggt tgg gtc aag cag atc gtc aac gat Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp	480		
145	150	155	160
ttc gtc atc gag gct aac aag tcc aac acc atg gac aag att gcc gac Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp	528		
165	170	175	
atc tcc ttg att gtc cca tac atc ggt ttg gcc ttg aac gtc ggt aac Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn	576		
180	185	190	
gag acc gcc aag ggt aac ttc gag aac gct ttc gag atc gct ggt gcc Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala	624		
195	200	205	
tcc atc ttg ttg gag ttc atc cca gag ttg ttg atc cca gtc gtc ggt Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly	672		
210	215	220	
gcc ttc ttg ttg gag tcc tac atc gac aac aag aac aag atc atc aag Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys	720		
225	230	235	240
acc atc gac aac gct ttg acc aag aga aac gag aag tgg tcc gac atg Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met	768		
245	250	255	
tac ggt ttg atc gtc gcc caa tgg ttg tcc acc gtc aac acc caa ttc Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe	816		
260	265	270	

Bf

tac acc atc aag gag ggt atg tac aag gcc ttg aac tac cag gcc caa 864
 Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
 275 280 285
 gct ttg gag gag atc atc aag tac aga tac aac atc tac tcc gag aag 912
 Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
 290 295 300
 gag aag tcc aac att aac atc gac ttc aac gac atc aac tcc aag ctg 960
 Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
 305 310 315 320
 aac gag ggt att aac cag gcc atc gac aac atc aac aac ttc atc aac 1008
 Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
 325 330 335
 ggt tgt tcc gtc tcc tac ttg atg aag aag atg att cca ttg gcc gtc 1056
 Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
 340 345 350
 gag aag ttg ttg gac ttc gac aac acc ctg aag aag aac ttg ttg aac 1104
 Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn
 355 360 365
 tac atc gac gag aac aag ttg tac ttg atc ggt tcc gct gag tac gag 1152
 Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
 370 375 380
 aag tcc aag gtc aac aag tac ttg aag acc atc atg cca ttc gac ttg 1200
 Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
 385 390 395 400
 tcc atc tac acc aac gac acc atc ttg atc gag atg ttc taa 1242
 Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
 405 410

<210> 22
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22
 Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
 1 5 10 15
 Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
 20 25 30
 Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
 35 40 45
 Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
 50 55 60
 Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
 65 70 75 80
 Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
 85 90 95
 Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
 100 105 110

Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
 115 120 125
 Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
 130 135 140
 Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
 145 150 155 160
 Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
 165 170 175
 Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
 180 185 190
 Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
 195 200 205
 Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
 210 215 220
 Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
 225 230 235 240
 Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
 245 250 255
 Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
 260 265 270
 Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
 275 280 285
 Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
 290 295 300
 Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
 305 310 315 320
 Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
 325 330 335
 Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
 340 345 350
 Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn
 355 360 365
 Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
 370 375 380
 Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
 385 390 395 400
 Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
 405 410

<210> 23
 <211> 1200
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1197)

<400> 23
 atg tcc ctg tac aac aag acc ctt gac tgt aga gag ctg ctg gtg aag 48
 Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1 5 10 15
 aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac 96
 Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
 20 25 30
 atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac 144

Ile	Phe	Leu	Arg	Lys	Asp	Ile	Asn	Glu	Glu	Thr	Glu	Val	Ile	Tyr	Tyr	
		35					40						45			
cca	gac	aac	gtg	tca	gta	gac	caa	gtg	atc	ctc	agt	aag	aac	acc	tcc	192
Pro	Asp	Asn	Val	Ser	Val	Asp	Gln	Val	Ile	Leu	Ser	Lys	Asn	Thr	Ser	
	50					55					60					
gag	cat	gga	caa	cta	gac	ctg	ctc	tac	cct	agt	atc	gac	agt	gag	agt	240
Glu	His	Gly	Gln	Leu	Asp	Leu	Leu	Tyr	Pro	Ser	Ile	Asp	Ser	Glu	Ser	
	65				70					75					80	
gag	atc	ctg	cca	ggg	gag	aat	caa	gtc	ttc	tac	gac	aac	cgt	acc	cag	288
Glu	Ile	Leu	Pro	Gly	Glu	Asn	Gln	Val	Phe	Tyr	Asp	Asn	Arg	Thr	Gln	
				85					90					95		
aac	gtg	gac	tac	ctg	aac	tcc	tac	tac	tac	cta	gag	tct	cag	aag	ctg	336
Asn	Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu	
			100					105					110			
agt	gac	aac	gtg	gag	gac	ttc	act	ttc	acg	cgt	tca	atc	gag	gag	gct	384
Ser	Asp	Asn	Val	Glu	Asp	Phe	Thr	Phe	Thr	Arg	Ser	Ile	Glu	Glu	Ala	
		115					120					125				
ctg	gac	aac	agt	gca	aag	gtg	tac	act	tac	ttc	cct	acc	ctg	gct	aac	432
Leu	Asp	Asn	Ser	Ala	Lys	Val	Tyr	Thr	Tyr	Phe	Pro	Thr	Leu	Ala	Asn	
	130					135					140					
aag	gtg	aat	gcc	ggt	gtg	caa	ggt	ggt	ctg	ttc	ctg	atg	tgg	gca	aac	480
Lys	Val	Asn	Ala	Gly	Val	Gln	Gly	Gly	Leu	Phe	Leu	Met	Trp	Ala	Asn	
	145				150				155					160		
gac	gtg	ggt	gag	gac	ttc	act	acc	aac	atc	ctg	cgt	aag	gac	aca	ctg	528
Asp	Val	Val	Glu	Asp	Phe	Thr	Thr	Asn	Ile	Leu	Arg	Lys	Asp	Thr	Leu	
			165					170						175		
gac	aag	atc	tca	gat	gtg	tca	gct	atc	atc	ccc	tac	atc	gga	ccc	gca	576
Asp	Lys	Ile	Ser	Asp	Val	Ser	Ala	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	
			180				185						190			
ctg	aac	atc	tcc	aac	tct	gtg	cgt	cgt	gga	aac	ttc	act	gag	gca	ttc	624
Leu	Asn	Ile	Ser	Asn	Ser	Val	Arg	Arg	Gly	Asn	Phe	Thr	Glu	Ala	Phe	
		195					200					205				
gca	gtc	act	ggt	gtc	acc	atc	ctg	ctg	gag	gca	ttc	cct	gag	ttc	aca	672
Ala	Val	Thr	Gly	Val	Thr	Ile	Leu	Leu	Glu	Ala	Phe	Pro	Glu	Phe	Thr	
	210					215				220						
atc	cct	gct	ctg	ggt	gca	ttc	gtg	atc	tac	agt	aag	gtc	cag	gag	cga	720
Ile	Pro	Ala	Leu	Gly	Ala	Phe	Val	Ile	Tyr	Ser	Lys	Val	Gln	Glu	Arg	
	225				230					235				240		
aac	gag	atc	atc	aag	acc	atc	gac	aac	tgt	ctg	gag	cag	agg	atc	aag	768
Asn	Glu	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Lys	
				245				250						255		
aga	tgg	aag	gac	tcc	tac	gag	tgg	atg	atg	gga	acg	tgg	ttg	tcc	agg	816
Arg	Trp	Lys	Asp	Ser	Tyr	Glu	Trp	Met	Met	Gly	Thr	Trp	Leu	Ser	Arg	
			260					265					270			
atc	atc	acc	cag	ttc	aac	aac	atc	tcc	tac	cag	atg	tac	gac	tcc	ctg	864
Ile	Ile	Thr	Gln	Phe	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Tyr	Asp	Ser	Leu	

B4

275

280

285

aac tac cag gca ggt gca atc aag gct aag atc gac ctg gag tac aag 912
 Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
 290 295 300

aag tac tcc gga agc gac aag gag aac atc aag agc cag gtt gag aac 960
 Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
 305 310 315 320

ctg aag aac agt ctg gac gtc aag atc tcg gag gca atg aac aac atc 1008
 Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
 325 330 335

aac aag ttc atc cga gag tgc tcc gtc acc tac ctg ttc aag aac atg 1056
 Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
 340 345 350

ctg cct aag gtc atc gac gag ctg aac gag ttc gac cga aac acc aag 1104
 Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
 355 360 365

gca aag ctg atc aac ctg atc gac tcc cat aac atc atc ctg gtc ggt 1152
 Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
 370 375 380

gag gtc gac aag ctg aag gca aag gta aac aac agc ttc cag aac 1197
 Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
 385 390 395

taa 1200

<210> 24

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1 5 10 15

Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
 20 25 30

Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
 35 40 45

Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
 50 55 60

Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
 65 70 75 80

Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
 85 90 95

Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Leu Glu Ser Gln Lys Leu
 100 105 110

Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
 115 120 125

Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
 130 135 140

Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
 145 150 155 160

Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
 165 170 175
 Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
 180 185 190
 Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
 195 200 205
 Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
 210 215 220
 Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
 225 230 235 240
 Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
 245 250 255
 Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
 260 265 270
 Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
 275 280 285
 Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
 290 295 300
 Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
 305 310 315 320
 Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
 325 330 335
 Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
 340 345 350
 Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
 355 360 365
 Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
 370 375 380
 Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
 385 390 395

<210> 25
 <211> 1161
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1158)

<400> 25
 atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac 48
 Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1 5 10 15
 aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc 96
 Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
 20 25 30
 gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac 144
 Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
 35 40 45
 aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac 192
 Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
 50 55 60
 cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg 240

Pro 65	Glu	Ile	Val	Asp	Pro 70	Leu	Leu	Pro	Asn	Val 75	Asn	Met	Glu	Pro	Leu 80	
aac	ttg	cca	ggt	gag	gag	atc	gtc	ttc	tac	gac	gac	atc	acc	aag	tac	288
Asn	Leu	Pro	Gly	Glu 85	Glu	Ile	Val	Phe	Tyr 90	Asp	Asp	Ile	Thr	Lys 95	Tyr	
gtc	gac	tac	ttg	aac	tcc	tac	tac	tac	ttg	gag	tct	caa	aag	ttg	tct	336
Val	Asp	Tyr	Leu 100	Asn	Ser	Tyr	Tyr	Tyr 105	Leu	Glu	Ser	Gln	Lys 110	Leu	Ser	
aac	aac	gtc	gag	aac	atc	acc	ttg	acc	acc	tcc	gtc	gag	gag	gcc	ttg	384
Asn	Asn	Val 115	Glu	Asn	Ile	Thr	Leu 120	Thr	Thr	Ser	Val	Glu 125	Glu	Ala	Leu	
ggt	tac	tct	aac	aag	atc	tac	acc	ttc	ctg	cca	tcc	ttg	gct	gag	aag	432
Gly	Tyr	Ser	Asn 130	Lys	Ile	Tyr	Thr 135	Phe	Leu	Pro	Ser	Leu 140	Ala	Glu	Lys	
gtt	aac	aag	ggt	gtt	caa	gct	ggt	ttg	ttc	ctg	aac	tgg	gcc	aac	gag	480
Val	Asn	Lys	Gly 145	Val	Gln	Ala	Gly 150	Leu	Phe	Leu 155	Asn	Trp	Ala	Asn	Glu 160	
gtc	gtc	gag	gac	ttc	acc	acc	aac	atc	atg	aag	aag	gac	acc	ctg	gac	528
Val	Val	Glu	Asp 165	Phe	Thr	Thr	Asn	Ile	Met	Lys 170	Lys	Asp	Thr	Leu	Asp 175	
aag	atc	tcc	gac	gtc	tcc	gtc	atc	atc	cca	tac	atc	ggt	cca	gcc	ttg	576
Lys	Ile	Ser	Asp 180	Val	Ser	Val	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	Leu 190	
aac	atc	ggt	aac	tcc	gcc	ctg	aga	ggt	aac	ttc	aac	cag	gcc	ttc	gcc	624
Asn	Ile	Gly 195	Asn	Ser	Ala	Leu	Arg 200	Gly	Asn	Phe	Asn	Gln	Ala	Phe	Ala	
acc	gcc	ggt	gtc	gcc	ttc	ctg	ctg	gag	ggt	ttc	cca	gag	ttc	acc	atc	672
Thr	Ala	Gly 210	Val	Ala	Phe	Leu	Glu 215	Gly	Phe	Pro	Glu	Phe	Thr	Ile		
cca	gcc	ctg	ggt	gtc	ttc	acc	ttc	tac	tcc	tcc	atc	cag	gag	aga	gag	720
Pro	Ala	Leu 225	Gly	Val	Phe	Thr	Phe 230	Tyr	Ser	Ser	Ile	Gln	Glu	Arg	Glu 240	
aag	atc	atc	aag	acc	atc	gag	aac	tgc	ttg	gag	cag	aga	gtc	aag	aga	768
Lys	Ile	Ile	Lys 245	Thr	Ile	Glu	Asn	Cys	Leu 250	Glu	Gln	Arg	Val	Lys	Arg 255	
tgg	aag	gac	tcc	tac	cag	tgg	atg	gtt	tcc	aac	tgg	ctg	tcc	aga	atc	816
Trp	Lys	Asp	Ser 260	Tyr	Gln	Trp	Met	Val	Ser	Asn	Trp	Leu	Ser	Arg	Ile	
acc	acc	caa	ttc	aac	cac	atc	aac	tac	cag	atg	tac	gac	tcc	ctg	tcc	864
Thr	Thr	Gln 275	Phe	Asn	His	Ile	Asn	Tyr	Gln	Met	Tyr	Asp	Ser	Leu	Ser	
tac	cag	gcc	gac	gcc	atc	aag	gcc	aag	atc	gac	ctg	gag	tac	aag	aag	912
Tyr	Gln	Ala 290	Asp	Ala	Ile	Lys	Ala 295	Lys	Ile	Asp	Leu	Glu	Tyr	Lys	Lys	
tac	tcc	ggt	tcc	gac	aag	gag	aac	atc	aag	tcc	cag	gtc	gag	aac	ctg	960
Tyr	Ser	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Lys	Ser	Gln	Val	Glu	Asn	Leu	

B4

Sub
Q1

305	310	315	320	
aag aac tcc ttg gac gtc aag atc tcc gag gcc atg aac aac atc aac				1008
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn				
325		330	335	
aag ttc atc cgt gag tgt tcc gtc acc tac ctg ttc aag aac atg ctg				1056
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu				
340		345	350	
cca aag gtc atc gac gag ctg aac aag ttc gac ctg aga acc aag acc				1104
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr				
355		360	365	
gag ctg atc aac ctg atc gac tcc cac aac atc atc ctg gtt ggt gag				1152
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu				
370		375	380	
gtt gac taa				1161
Val Asp				
385				

<210> 26
 <211> 386
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 26

Met	Ala	Asn	Ser	Arg	Asp	Asp	Ser	Thr	Cys	Ile	Lys	Val	Lys	Asn	Asn
1				5					10					15	
Arg	Leu	Pro	Tyr	Val	Ala	Asp	Lys	Asp	Ser	Ile	Ser	Gln	Glu	Ile	Phe
			20					25					30		
Glu	Asn	Lys	Ile	Ile	Thr	Asp	Glu	Thr	Asn	Val	Gln	Asn	Tyr	Ser	Asp
		35					40					45			
Lys	Phe	Ser	Leu	Asp	Glu	Ser	Ile	Leu	Asp	Gly	Gln	Val	Pro	Ile	Asn
	50					55				60					
Pro	Glu	Ile	Val	Asp	Pro	Leu	Leu	Pro	Asn	Val	Asn	Met	Glu	Pro	Leu
65					70					75				80	
Asn	Leu	Pro	Gly	Glu	Glu	Ile	Val	Phe	Tyr	Asp	Asp	Ile	Thr	Lys	Tyr
			85						90					95	
Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu	Ser
			100					105					110		
Asn	Asn	Val	Glu	Asn	Ile	Thr	Leu	Thr	Thr	Ser	Val	Glu	Glu	Ala	Leu
		115					120					125			
Gly	Tyr	Ser	Asn	Lys	Ile	Tyr	Thr	Phe	Leu	Pro	Ser	Leu	Ala	Glu	Lys
	130					135					140				
Val	Asn	Lys	Gly	Val	Gln	Ala	Gly	Leu	Phe	Leu	Asn	Trp	Ala	Asn	Glu
145					150				155					160	
Val	Val	Glu	Asp	Phe	Thr	Thr	Asn	Ile	Met	Lys	Lys	Asp	Thr	Leu	Asp
			165						170					175	
Lys	Ile	Ser	Asp	Val	Ser	Val	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	Leu
			180					185					190		
Asn	Ile	Gly	Asn	Ser	Ala	Leu	Arg	Gly	Asn	Phe	Asn	Gln	Ala	Phe	Ala
		195					200					205			
Thr	Ala	Gly	Val	Ala	Phe	Leu	Leu	Glu	Gly	Phe	Pro	Glu	Phe	Thr	Ile
	210					215					220				
Pro	Ala	Leu	Gly	Val	Phe	Thr	Phe	Tyr	Ser	Ser	Ile	Gln	Glu	Arg	Glu

B4

See C.

225 230 235 240
 Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
 Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
 Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
 Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
 Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
 Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
 Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
 Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
 Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
 Val Asp
 385

<210> 27
 <211> 1149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1146)

<400> 27
 atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct 48
 Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
 1 5 10 15
 tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att 96
 Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
 20 25 30
 gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag 144
 Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
 35 40 45
 gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag 192
 Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
 50 55 60
 aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac 240
 Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
 65 70 75 80
 tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac 288
 Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
 85 90 95
 gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac 336
 Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn

Sub
 C

	100	105	110	
	gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag			384
	Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys			
	115	120	125	
	atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct			432
	Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro			
	130	135	140	
	gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac			480
	Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp			
	145	150	155	160
	ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac			528
	Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp			
	165	170	175	
	atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac			576
	Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn			
	180	185	190	
	gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc			624
	Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala			
	195	200	205	
	ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg			672
	Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu			
	210	215	220	
	gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag			720
	Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys			
	225	230	235	240
	gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg			768
	Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp			
	245	250	255	
	aag gaa gtc tat tcc ttc atc gtc tcc aac tgg atg acc aag atc aac			816
	Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn			
	260	265	270	
	acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac			864
	Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn			
	275	280	285	
	cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac			912
	Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr			
	290	295	300	
	acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag			960
	Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln			
	305	310	315	320
	atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc			1008
	Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile			
	325	330	335	
	gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc			1056
	Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile			
	340	345	350	

B4

Sub
C1

aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag 1104
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
355 360 365

acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg 1146
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
370 375 380

taa 1149

<210> 28

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 28

Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
1 5 10 15
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
20 25 30
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
35 40 45
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
50 55 60
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65 70 75 80
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
85 90 95
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
100 105 110
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
115 120 125
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
130 135 140
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145 150 155 160
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
165 170 175
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
180 185 190
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
195 200 205
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
210 215 220
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225 230 235 240
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
245 250 255
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
260 265 270
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
275 280 285
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
290 295 300
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305 310 315 320
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile

325 330 335
 Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
 340 345 350
 Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
 355 360 365
 Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
 370 375 380

<210> 29

<211> 1227

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<221> CDS

<222> (1)...(1224)

<400> 29

atg gcc cca cca cgt ctg tgt att aga gtc aac aac tca gaa tta ttc 48
 Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1 5 10 15
 ttt gtc gct tcc gag tca agc tac aac gag aac gat att aac aca cct 96
 Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
 20 25 30
 aaa gag att gac gat act acc aac cta aac aac aac tac cgg aac aac 144
 Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
 35 40 45
 ttg gat gag gtt att ttg gat tac aac tca cag acc atc cct caa att 192
 Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
 50 55 60
 tcc aac cgt acc tta aac act ctt gtc caa gac aac tcc tac gtt cca 240
 Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65 70 75 80
 aga tac gat tct aac ggt acc tca gag atc gag gag tat gat gtt gtt 288
 Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
 85 90 95
 gac ttt aac gtc ttt ttc tat ttg cat gcc cag aag gtg cca gaa ggt 336
 Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
 100 105 110
 gaa acc aac atc tca ttg act tct tcc att gat acc gcc ttg ttg gaa 384
 Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
 115 120 125
 gag tcc aag gat atc ttc ttt tct tcg gag ttt atc gat act atc aac 432
 Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
 130 135 140
 aag cct gtc aac gcc gct ctg ttc att gat tgg att agc aag gtc atc 480
 Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
 145 150 155 160

B4
 Sub
 Cy

aga gat ttt acc act gaa gct act caa aag tcc act gtt gat aag att	528
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile	
165 170 175	
gct gac atc tct ttg att gtc ccc tat gtc ggt ctt gct ttg aac atc	576
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile	
180 185 190	
att att gag gca gaa aag ggt aac ttt gag gag gct ttt gaa ttg ttg	624
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu	
195 200 205	
gga gtt ggt att ttg ttg gag ttt gtt cca gaa ctt acc att cct gtc	672
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val	
210 215 220	
att tta gtt ttt acg atc aag tcc tac atc gat tca tac gag aac aag	720
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys	
225 230 235 240	
aat aaa gca att aaa gct att aac aac tcc ttg atc gaa aga gag gct	768
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala	
245 250 255	
aag tgg aag gaa atc tac tca tgg att gta tca aac tgg ctt act aga	816
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg	
260 265 270	
att aac act caa ttt aac aag aga aag gag caa atg tac cag gct ctg	864
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu	
275 280 285	
caa aac caa gtc gat gct atc aag act gca att gaa tac aag tac aac	912
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn	
290 295 300	
aac tat act tcc gat gag aag aac aga ctt gaa tct gaa tac aat atc	960
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile	
305 310 315 320	
aac aac att gaa gaa gag ttg aac aag aaa gtt tct ttg gct atg aag	1008
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys	
325 330 335	
aat atc gaa aga ttt atg acc gaa tcc tct atc tct tac ttg atg aag	1056
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys	
340 345 350	
ttg atc aat gag gcc aag gtt ggt aag ttg aag aag tac gat aac cac	1104
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His	
355 360 365	
gtt aag agc gat ctg ctg aac tac att ctc gac cac aga tca atc ctg	1152
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu	
370 375 380	
gga gag cag aca aac gag ctg agt gat ttg gtt act tcc act ttg aac	1200
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn	
385 390 395 400	
tcc tcc att cca ttt gag ctt tct taa	1227

B4

Sub
C.Y

Ser Ser Ile Pro Phe Glu Leu Ser
405

<210> 30
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
1 5 10 15
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
20 25 30
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
35 40 45
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
50 55 60
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
65 70 75 80
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
85 90 95
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
100 105 110
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
115 120 125
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
130 135 140
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
145 150 155 160
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile
165 170 175
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile
180 185 190
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu
195 200 205
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val
210 215 220
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys
225 230 235 240
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala
245 250 255
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg
260 265 270
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
275 280 285
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
290 295 300
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
305 310 315 320
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
325 330 335
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
340 345 350
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
355 360 365
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
370 375 380

B4
Sub
Cy

Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
 385 390 395 400
 Ser Ser Ile Pro Phe Glu Leu Ser
 405

<210> 31
 <211> 1233
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1230)

<400> 31
 atg gcc aaa aat acc ggt aaa tct gaa cag tgt att att gtt aat aat 48
 Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1 5 10 15
 gag gat tta ttt ttc ata gct aat aaa gat agt ttt tca aaa gat tta 96
 Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
 20 25 30
 gct aaa gca gaa act ata gca tat aat aca caa aat aat act ata gaa 144
 Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
 35 40 45
 aat aat ttt tct ata gat cag ttg att tta gat aat gat tta agc agt 192
 Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
 50 55 60
 ggc ata gac tta cca aat gaa aac aca gaa cca ttt aca aat ttt gac 240
 Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
 65 70 75 80
 gac ata gat atc cct gtg tat att aaa caa tct gct tta aaa aaa att 288
 Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
 85 90 95
 ttt gtg gat gga gat agc ctt ttt gaa tat tta cat gct caa aca ttt 336
 Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
 100 105 110
 cct tct aat ata gaa aat cta caa cta acg aat tca tta aat gat gct 384
 Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
 115 120 125
 tta aga aat aat aat aaa gtc tat act ttt ttt tct aca aac ctt gtt 432
 Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
 130 135 140
 gaa aaa gct aat aca gtt gta ggt gct tca ctt ttt gta aac tgg gta 480
 Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
 145 150 155 160
 aaa gga gta ata gat gat ttt aca tct gaa tcc aca caa aaa agt act 528
 Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
 165 170 175

B4

Sub
 C1

ata gat aaa gtt tca gat gta tcc ata att att ccc tat ata gga cct	576
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro	
180 185 190	
gct ttg aat gta gga aat gaa aca gct aaa gaa aat ttt aaa aat gct	624
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala	
195 200 205	
ttt gaa ata ggt gga gcc gct atc tta atg gag ttt att cca gaa ctt	672
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu	
210 215 220	
att gta cct ata gtt gga ttt ttt aca tta gaa tca tat gta gga aat	720
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn	
225 230 235 240	
aaa ggg cat att att atg acg ata tcc aat gct tta aag aaa agg gat	768
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp	
245 250 255	
caa aaa tgg aca gat atg tat ggt ttg ata gta tcg cag tgg ctc tca	816
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser	
260 265 270	
acg gtt aat act caa ttt tat aca ata aaa gaa aga atg tac aat gct	864
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala	
275 280 285	
tta aat aat caa tca caa gca ata gaa aaa ata ata gaa gat caa tat	912
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr	
290 295 300	
aat aga tat agt gaa gaa gat aaa atg aat att aac att gat ttt aat	960
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn	
305 310 315 320	
gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat	1008
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn	
325 330 335	
ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga	1056
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg	
340 345 350	
atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt	1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu	
355 360 365	
aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt	1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu	
370 375 380	
gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac	1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp	
385 390 395 400	
agt ata cca ttt gat ctt tca cta tat acc taa	1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr	
405 410	

B4

Sub
C1

<210> 32
 <211> 410
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32
 Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1 5 10 15
 Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
 20 25 30
 Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
 35 40 45
 Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
 50 55 60
 Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
 65 70 75 80
 Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
 85 90 95
 Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
 100 105 110
 Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
 115 120 125
 Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
 130 135 140
 Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
 145 150 155 160
 Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
 165 170 175
 Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
 180 185 190
 Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
 195 200 205
 Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
 210 215 220
 Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
 225 230 235 240
 Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
 245 250 255
 Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
 260 265 270
 Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala
 275 280 285
 Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr
 290 295 300
 Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn
 305 310 315 320
 Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn
 325 330 335
 Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg
 340 345 350
 Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
 355 360 365
 Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
 370 375 380
 Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
 385 390 395 400
 Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr

B4

<210> 33
 <211> 1314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (10)...(1305)

<400> 33
 gaattcagc atg tct tac act aac gac aaa atc ctg atc ctg tac ttc aac 51
 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
 1 5 10

aaa ctg tac aaa aaa atc aaa gac aac tct atc ctg gac atg cgt tac 99
 Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15 20 25 30

gaa aac aac aaa ttc atc gac atc tct ggc tat ggt tct aac atc tct 147
 Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
 35 40 45

atc aac ggt gac gtc tac atc tac tct act aac cgc aac cag ttc ggt 195
 Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
 50 55 60

atc tac tct tct aaa ccg tct gaa gta aac atc gct cag aac aac gac 243
 Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
 65 70 75

atc atc tac aac ggt cgt tac cag aac ttc tct atc tct ttc tgg gtt 291
 Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
 80 85 90

cgt atc ccg aaa tac ttc aac aaa gtt aac ctg aac aac gaa tac act 339
 Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
 95 100 105 110

atc atc gac tgc atc cgt aac aac aac tct ggt tgg aaa atc tct ctg 387
 Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
 115 120 125

aac tac aac aaa atc atc tgg act ctg cag gac act gct ggt aac aac 435
 Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
 130 135 140

cag aaa ctg gtt ttc aac tac act cag atg atc tct atc tct gac tac 483
 Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
 145 150 155

att aat aaa tgg atc ttc gtt act atc act aac aac cgt ctg ggt aac 531
 Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
 160 165 170

tct cgt atc tac atc aac ggt aac ctg atc gat gaa aaa tct atc tct 579
 Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser

B4
 Sub
 Cys

175	180	185	190	
aac ctg ggt gac atc cac gtt tct gac aac atc ctg ttc aaa atc gtt	Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val	627		
	195 200 205			
ggt tgc aac gac acg cgt tac gtt ggt atc cgt tac ttc aaa gtt ttc	Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe	675		
	210 215 220			
gac act gaa ctg ggt aaa act gaa atc gaa act ctg tac tct gac gaa	Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu	723		
	225 230 235			
ccg gac ccg tct atc ctg aaa gac ttc tgg ggt aac tac ctg ctg tac	Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr	771		
	240 245 250			
aac aaa cgt tac tac ctg ctg aac ctg ctc cgg act gac aaa tct atc	Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile	819		
	255 260 265 270			
act cag aac tct aac ttc ctg aac atc aac cag cag cgt ggt gtt tat	Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr	867		
	275 280 285			
cag aaa cct aat atc ttc tct aac act cgt ctg tac act ggt gtt gaa	Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu	915		
	290 295 300			
gtt atc atc cgt aaa aac ggt tct act gac atc tct aac act gac aac	Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn	963		
	305 310 315			
ttc gta cgt aaa aac gac ctg gct tac atc aac gtt gtt gac cgt gac	Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp	1011		
	320 325 330			
gtt gaa tac cgt ctg tac gct gac atc tct atc gct aaa ccg gaa aaa	Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys	1059		
	335 340 345 350			
atc atc aaa ctg atc cgt act tct aac tct aac aac tct ctg ggt cag	Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln	1107		
	355 360 365			
atc atc gtt atg gac tcg atc ggt aac aac tgc act atg aac ttc cag	Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln	1155		
	370 375 380			
aac aac aac ggt ggt aac atc ggt ctg ctg ggt ttc cac tct aac aac	Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn	1203		
	385 390 395			
ctg gtt gct tct tca tgg tac tac aac aac atc cgt aaa aac act tct	Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser	1251		
	400 405 410			
tct aac ggt tgc ttc tgg tct ttc atc tct aaa gaa cac ggt tgg cag	Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln	1299		
	415 420 425 430			

B4

Sub C1

gaa aac taagaattc
Glu Asn

1314

<210> 34
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
1 5 10 15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
20 25 30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
35 40 45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
50 55 60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65 70 75 80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
85 90 95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
100 105 110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
115 120 125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
130 135 140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145 150 155 160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
165 170 175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
180 185 190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
195 200 205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
210 215 220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225 230 235 240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
245 250 255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
260 265 270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
275 280 285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
290 295 300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305 310 315 320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
325 330 335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
340 345 350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
355 360 365

B4

Sub
C17

Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
370 375 380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385 390 395 400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
405 410 415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
420 425 430

B4
Sub C